

Pro Glu Ala Pro Ala Val Phe Ser Pro Glu Gly Thr Val Leu Leu Thr
 1345 1350 1355 1360

Gly Gly Thr Gly Ser Leu Gly Gly Leu Val Ala Lys His Leu Val Ala
 1365 1370 1375

Arg His Gly Val Arg Arg Leu Val Leu Ala Ser Arg Arg Gly Val Ala
 1380 1385 1390

Ala Glu Asp Leu Val Thr Glu Leu Thr Glu Gln Gly Ala Thr Val Ser
 1395 1400 1405

Val Val Ala Cys Asp Val Ser Asp Arg Asp Gln Val Ala Ala Leu Leu
 1410 1415 1420

Ala Glu His Arg Pro Thr Gly Ile Val His Leu Ala Gly Leu Leu Asp
 1425 1430 1435 1440

Asp Gly Val Ile Gly Ala Leu Asn Arg Glu Arg Leu Ala Gly Val Phe
 1445 1450 1455

Ala Pro Lys Val Asp Ala Val Gln His Leu Asp Glu Leu Thr Arg Asp
 1460 1465 1470

Leu Gly Leu Asp Ala Phe Val Val Phe Ser Ser Ala Ala Ala Leu Met
 1475 1480 1485

Gly Ser Ala Gly Gln Gly Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp
 1490 1495 1500

Gly Leu Met Ala Gly Arg Arg Ala Ala Gly Leu Pro Gly Val Ser Leu
 1505 1510 1515 1520

Ala Trp Gly Leu Trp Glu Gln Ala Asp Gly Leu Thr Ala Asn Leu Ser
 1525 1530 1535

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Ala Thr Asp Gln Ala Arg Met Ser Arg Gly Gly Val Leu Pro Met Thr
 1540 1545 1550

Pro Ala Glu Ala Leu Asp Ile Phe Asp Ile Gly Leu Ala Ala Glu Gln
 1555 1560 1565

Ala Leu Leu Val Pro Ile Lys Leu Asp Leu Arg Thr Leu Arg Gly Gln
 1570 1575 1580

Ala Thr Ala Gly Gly Glu Val Pro His Leu Leu Arg Gly Leu Val Arg
 1585 1590 1595 1600

Ala Ser Arg Arg Val Thr Arg Thr Ala Ala Ala Ser Gly Gly Gly Gly
 1605 1610 1615

Leu Val His Lys Leu Ala Gly Arg Pro Ala Glu Glu Gln Glu Ala Val
 1620 1625 1630

Leu Leu Gly Ile Val Gln Ala Glu Ala Ala Ala Val Leu Gly Phe Asn
 1635 1640 1645

Ala Pro Glu Leu Ala Gln Gly Thr Arg Gly Phe Ser Asp Leu Gly Phe
 1650 1655 1660

Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu Ser Ala Ala Thr
 1665 1670 1675 1680

Gly Val Lys Leu Pro Ala Thr Leu Val Phe Asp Tyr Pro Thr Pro Val
 1685 1690 1695

Ala Leu Ala Arg His Leu Arg Glu Glu Leu Gly Glu Thr Val Ala Gly
 1700 1705 1710

Ala Pro Ala Thr Pro Val Thr Thr Val Ala Asp Ala Gly Glu Pro Ile
 1715 1720 1725

Ala Ile Val Gly Met Ala Cys Arg Leu Pro Gly Gly Val Met Ser Pro

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1730	1735	1740	
Asp Asp Leu Trp Arg Met Val Ala Glu Gly Arg Asp Gly Met Ser Pro			
1745	1750	1755	1760
Phe Pro Gly Asp Arg Gly Trp Asp Leu Asp Gly Leu Phe Asp Ser Asp			
1765	1770	1775	
Pro Glu Arg Pro Gly Thr Ala Tyr Ile Arg Gln Gly Gly Phe Leu His			
1780	1785	1790	
Glu Ala Ala Leu Phe Asp Pro Gly Phe Phe Gly Ile Ser Pro Arg Glu			
1795	1800	1805	
Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Ala Ser Trp			
1810	1815	1820	
Glu Ala Leu Glu Arg Ala Gly Ile Asp Pro Thr Lys Ala Arg Gly Asp			
1825	1830	1835	1840
Ala Val Gly Val Phe Ser Gly Val Ser Ile His Asp Tyr Leu Glu Ser			
1845	1850	1855	
Leu Ser Asn Met Pro Ala Glu Leu Glu Gly Phe Val Thr Thr Ala Thr			
1860	1865	1870	
Ala Gly Ser Val Ala Ser Gly Arg Val Ser Tyr Thr Phe Gly Phe Glu			
1875	1880	1885	
Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala			
1890	1895	1900	
Ile His Leu Ala Ala Gln Ala Leu Arg Gln Gly Glu Cys Thr Met Ala			
1905	1910	1915	1920
Leu Ala Gly Gly Val Ala Val Met Gly Ser Pro Ile Gly Val Ile Gly			
1925	1930	1935	

Met Ser Arg Gln Arg Gly Met Ala Glu Asp Gly Arg Val Lys Ala Phe
 1940 1945 1950

Ala Asp Gly Ala Asp Gly Thr Val Leu Ser Glu Gly Val Gly Ile Val
 1955 1960 1965

Val Leu Glu Arg Leu Ser Val Ala Arg Glu Arg Gly His Arg Val Leu
 1970 1975 1980

Ala Val Leu Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly
 1985 1990 1995 2000

Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Ser Ala
 2005 2010 2015

Leu Ala Gly Ala Gly Leu Gln Pro Ser Glu Val Asp Val Val Glu Ala
 2020 2025 2030

His Gly Thr Gly Thr Ala Leu Gly Glu Pro Ile Glu Ala Gln Ala Leu
 2035 2040 2045

Leu Ala Thr Tyr Gly Lys Ser Arg Glu Thr Pro Leu Trp Leu Gly Ser
 2050 2055 2060

Leu Lys Ser Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala Ala
 2065 2070 2075 2080

Val Ile Lys Met Val Gln Ala Leu Arg Gln Asp Thr Leu Pro Pro Thr
 2085 2090 2095

Leu His Val Gln Glu Pro Thr Lys Gln Val Asp Trp Ser Ala Gly Ala
 2100 2105 2110

Val Glu Leu Leu Thr Glu Gly Arg Glu Trp Ala Arg Asn Gly His Pro
 2115 2120 2125

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Arg Arg Ala Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His
 2130 2135 2140

Leu Ile Leu Glu Glu Ala Pro Ala Asp Asp Thr Ala Glu Ala Asp Val
 2145 2150 2155 2160

Pro Asp Ala Val Val Pro Val Val Ile Ser Ala Arg Ser Thr Gly Ser
 2165 2170 2175

Leu Ala Gly Gln Ala Gly Arg Leu Ala Ala Phe Leu Asp Gly Asp Val
 2180 2185 2190

Pro Leu Thr Arg Val Ala Gly Ala Leu Leu Ser Thr Arg Ala Thr Leu
 2195 2200 2205

Thr Asp Arg Ala Val Val Val Ala Gly Ser Ala Glu Glu Ala Arg Ala
 2210 2215 2220

Gly Leu Thr Ala Leu Ala Arg Gly Glu Ser Ala Ser Gly Leu Val Thr
 2225 2230 2235 2240

Gly Thr Ala Gly Met Pro Gly Lys Thr Val Trp Val Phe Pro Gly Gln
 2245 2250 2255

Gly Thr Gln Trp Ala Gly Met Gly Arg Glu Leu Leu Glu Ala Ser Pro
 2260 2265 2270

Val Phe Ala Glu Arg Ile Glu Glu Cys Ala Ala Ala Leu Gln Pro Trp
 2275 2280 2285

Ile Asp Trp Ser Leu Leu Asp Val Leu Arg Gly Glu Gly Glu Leu Asp
 2290 2295 2300

Arg Val Asp Val Leu Gln Pro Ala Cys Phe Ala Val Met Val Gly Leu
 2305 2310 2315 2320

Ala Ala Val Trp Ala Ser Val Gly Val Val Pro Asp Ala Val Leu Gly

2325	2330	2335
His Ser Gln Gly Glu Ile Ala Ala Ala Cys Val Ser Gly Ala Leu Ser		
2340	2345	2350
Leu Glu Asp Ala Ala Lys Val Val Ala Leu Arg Ser Gln Ala Ile Ala		
2355	2360	2365
Ala Glu Leu Ser Gly Arg Gly Gly Met Ala Ser Ile Gln Leu Ser His		
2370	2375	2380
Asp Glu Val Ala Ala Arg Leu Ala Pro Trp Ala Gly Arg Val Glu Ile		
2385	2390	2395
2400		
Ala Ala Val Asn Gly Pro Ala Ser Val Val Ile Ala Gly Asp Ala Glu		
2405	2410	2415
Ala Leu Thr Glu Ala Val Glu Val Leu Gly Gly Arg Arg Val Ala Val		
2420	2425	2430
Asp Tyr Ala Ser His Thr Arg His Val Glu Asp Ile Gln Asp Thr Leu		
2435	2440	2445
Ala Glu Thr Leu Ala Gly Ile Asp Ala Gln Ala Pro Val Val Pro Phe		
2450	2455	2460
Tyr Ser Thr Val Ala Gly Glu Trp Ile Thr Asp Ala Gly Val Val Asp		
2465	2470	2475
2480		
Gly Gly Tyr Trp Tyr Arg Asn Leu Arg Asn Gln Val Gly Phe Gly Pro		
2485	2490	2495
Ala Val Ala Glu Leu Ile Glu Gln Gly His Gly Val Phe Val Glu Val		
2500	2505	2510
Ser Ala His Pro Val Leu Val Gln Pro Ile Ser Glu Leu Thr Asp Ala		
2515	2520	2525

Val Val Thr Gly Thr Leu Arg Arg Asp Asp Gly Gly Val Arg Arg Leu
2530 2535 2540

Leu Thr Ser Met Ala Glu Leu Phe Val Arg Gly Val Pro Val Asp Trp
2545 2550 2555 2560

Ala Thr Met Ala Pro Pro Ala Arg Val Glu Leu Pro Thr Tyr Ala Phe
2565 2570 2575

Asp His Glu His Phe Trp Leu Ser Pro Pro Ala Val Ala Asp Ala Pro
2580 2585 2590

Ala Leu Gly Leu Ala Gly Ala Asp His Pro Leu Leu Gly Ala Val Leu
2595 2600 2605

Pro Leu Pro Gln Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Val
2610 2615 2620

Arg Thr His Pro Trp Leu Ala Asp Gly Val Pro Ala Ala Ala Leu Val
2625 2630 2635 2640

Glu Leu Ala Val Arg Ala Gly Asp Glu Ala Gly Cys Pro Val Leu Ala
2645 2650 2655

Asp Leu Thr Val Glu Lys Leu Leu Val Leu Pro Glu Ser Gly Gly Leu
2660 2665 2670

Arg Val Glu Val Ile Val Ser Gly Glu Arg Thr Val Glu Val Tyr Ser
2675 2680 2685

Gln Leu Glu Gly Ala Glu Asp Trp Ile Arg Asn Ala Thr Gly His Leu
2690 2695 2700

Ser Ala Thr Ala Pro Ala His Glu Ala Phe Asp Phe Thr Ala Trp Pro
2705 2710 2715 2720

Pro Ala Gly Ala Gln Gln Val Asp Gly Leu Trp Arg Arg Gly Asp Glu
 2725 2730 2735

Ile Phe Ala Glu Val Ala Leu Pro Glu Glu Leu Asp Ala Gly Ala Phe
 2740 2745 2750

Gly Ile His Pro Phe Leu Leu Asp Ala Ala Val Gln Pro Val Leu Ala
 2755 2760 2765

Asp Asp Glu Gln Pro Ala Glu Trp Arg Ser Leu Val Leu His Ala Ala
 2770 2775 2780

Gly Ala Ser Ala Leu Arg Val Arg Leu Val Pro Gly Gly Ala Leu Gln
 2785 2790 2795 2800

Ala Ala Asp Glu Thr Gly Gly Leu Val Leu Thr Ala Asp Ser Val Ala
 2805 2810 2815

Gly Arg Glu Leu Ser Ala Gly Lys Thr Arg Ala Gly Ser Leu Tyr Arg
 2820 2825 2830

Val Asp Trp Thr Glu Val Ser Ile Ala Asp Ser Ala Val Pro Ala Asn
 2835 2840 2845

Ile Glu Val Val Glu Ala Phe Gly Glu Glu Pro Leu Glu Leu Thr Gly
 2850 2855 2860

Arg Val Leu Glu Ala Val Gln Thr Trp Leu Val Thr Ala Ala Asp Asp
 2865 2870 2875 2880

Ala Arg Leu Val Val Val Thr Arg Gly Ala Val Arg Glu Val Thr Asp
 2885 2890 2895

Pro Ala Gly Ala Ala Val Trp Gly Leu Val Arg Ala Ala Gln Ala Glu
 2900 2905 2910

Asn Pro Gly Arg Ile Phe Leu Ile Asp Thr Asp Gly Glu Ile Pro Ala

2915	2920	2925
Leu Thr Gly Asp Glu Pro Glu Ile Ala Val Arg Gly Gly Lys Phe Phe		
2930	2935	2940
Val Pro Arg Ile Thr Arg Ala Glu Pro Ser Gly Ala Ala Val Phe Arg		
2945	2950	2955
		2960
Pro Asp Gly Thr Val Leu Ile Ser Gly Ala Gly Ala Leu Gly Gly Leu		
2965	2970	2975
Val Ala Arg Arg Leu Val Glu Arg His Gly Val Arg Lys Leu Val Leu		
2980	2985	2990
Ala Ser Arg Arg Gly Arg Asp Ala Asp Gly Val Ala Asp Leu Val Ala		
2995	3000	3005
Asp Leu Ala Ala Asp Val Ser Val Val Ala Cys Asp Val Ser Asp Arg		
3010	3015	3020
Ala Gln Val Ala Ala Leu Leu Asp Glu His Arg Pro Thr Ala Val Val		
3025	3030	3035
		3040
His Thr Ala Gly Val Ile Asp Ala Gly Val Ile Glu Thr Leu Asp Arg		
3045	3050	3055
Asp Arg Leu Ala Thr Val Phe Ala Pro Lys Val Asp Ala Val Arg His		
3060	3065	3070
Leu Asp Glu Leu Thr Arg Asp Arg Asp Leu Asp Ala Phe Val Val Tyr		
3075	3080	3085
Ser Ser Val Ser Ala Val Phe Met Gly Ala Gly Ser Gly Ser Tyr Ala		
3090	3095	3100
Ala Ala Asn Ala Phe Leu Asp Gly Leu Met Ala Asn Arg Arg Ala Ala		
3105	3110	3115
		3120

Gly Leu Pro Gly Leu Ser Leu Ala Trp Gly Leu Trp Asp Gln Ser Thr
 3125 3130 3135

Gly Met Ala Ala Gly Thr Asp Glu Ala Thr Arg Ala Arg Met Ser Arg
 3140 3145 3150

Arg Gly Gly Leu Gln Ile Met Thr Gln Ala Glu Gly Met Asp Leu Phe
 3155 3160 3165

Asp Ala Ala Leu Ser Ser Ala Glu Ser Leu Leu Val Pro Ala Lys Leu
 3170 3175 3180

Asp Leu Arg Gly Val Arg Ala Asp Ala Ala Ala Gly Gly Val Val Pro
 3185 3190 3195 3200

His Met Leu Arg Gly Leu Val Arg Ala Gly Arg Ala Gln Ala Arg Ala
 3205 3210 3215

Ala Ser Thr Val Asp Asn Gly Leu Ala Gly Arg Leu Ala Gly Leu Ala
 3220 3225 3230

Pro Ala Asp Gln Leu Thr Leu Leu Leu Asp Leu Val Arg Ala Gln Val
 3235 3240 3245

Ala Ala Val Leu Gly His Ala Asp Ala Ser Ala Val Arg Val Asp Thr
 3250 3255 3260

Ala Phe Lys Asp Ala Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg
 3265 3270 3275 3280

Asn Arg Met Arg Thr Ala Thr Gly Leu Lys Leu Pro Ala Thr Leu Val
 3285 3290 3295

Phe Asp Tyr Pro Asn Pro Gln Ala Leu Ala Arg His Leu Arg Asp Glu
 3300 3305 3310

Leu Gly Gly Ala Ala Gln Thr Pro Val Thr Thr Ala Ala Ala Lys Ala
 3315 3320 3325

Asp Leu Asp Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Leu Pro
 3330 3335 3340

Gly Gly Val Ala Gly Pro Glu Asp Leu Trp Arg Leu Val Ala Glu Gly
 3345 3350 3355 3360

Arg Asp Ala Val Ser Ser Phe Pro Thr Asp Arg Gly Trp Asp Thr Asp
 3365 3370 3375

Ser Leu Tyr Asp Pro Asp Pro Ala Arg Pro Gly Lys Thr Tyr Thr Arg
 3380 3385 3390

His Gly Gly Phe Leu His Glu Ala Gly Leu Phe Asp Ala Gly Phe Phe
 3395 3400 3405

Gly Ile Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu
 3410 3415 3420

Leu Leu Glu Ala Ser Trp Glu Ala Met Glu Asp Ala Gly Val Asp Pro
 3425 3430 3435 3440

Leu Ser Leu Lys Gly Asn Asp Val Gly Val Phe Thr Gly Met Phe Gly
 3445 3450 3455

Gln Gly Tyr Val Ala Pro Gly Asp Ser Val Val Thr Pro Glu Leu Glu
 3460 3465 3470

Gly Phe Ala Gly Thr Gly Gly Ser Ser Ser Val Ala Ser Gly Arg Val
 3475 3480 3485

Ser Tyr Val Phe Gly Phe Glu Gly Pro Ala Val Thr Ile Asp Ser Ala
 3490 3495 3500

Cys Ser Ser Ser Leu Val Ala Met His Leu Ala Ala Gln Ser Leu Arg

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3505	3510	3515	3520
Gln Gly Glu Cys Ser Met Ala Leu Ala Gly Gly Ala Thr Val Met Ala			
	3525	3530	3535
Asn Pro Gly Ala Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Val			
	3540	3545	3550
Asp Gly Arg Cys Lys Ala Phe Ala Ala Ala Ala Asp Gly Thr Gly Trp			
	3555	3560	3565
Ala Glu Gly Val Gly Val Val Ile Leu Glu Arg Leu Ser Val Ala Arg			
	3570	3575	3580
Glu Arg Gly His Arg Ile Leu Ala Val Leu Arg Gly Ser Ala Val Asn			
3585	3590	3595	3600
Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln			
	3605	3610	3615
Gln Arg Val Ile Arg Arg Ala Leu Val Ser Ala Gly Leu Ala Pro Ser			
	3620	3625	3630
Asp Val Asp Val Val Glu Ala His Gly Thr Gly Thr Thr Leu Gly Asp			
	3635	3640	3645
Pro Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Lys Asp Arg Glu			
	3650	3655	3660
Ser Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln			
3665	3670	3675	3680
Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Gln Ala Leu Arg			
	3685	3690	3695
His Glu Val Leu Pro Pro Thr Leu His Val Asp Arg Pro Thr Pro Glu			
	3700	3705	3710

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Val Asp Trp Ser Ala Gly Ala Val Glu Leu Leu Thr Glu Ala Arg Glu
 3715 3720 3725

Trp Pro Arg Asn Gly Arg Pro Arg Arg Ala Gly Val Ser Ala Phe Gly
 3730 3735 3740

Val Ser Gly Thr Asn Ala His Leu Ile Leu Glu Glu Ala Pro Ala Glu
 3745 3750 3755 3760

Glu Pro Val Pro Thr Pro Glu Val Pro Leu Val Pro Val Val Val Ser
 3765 3770 3775

Ala Arg Ser Arg Ala Ser Leu Ala Gly Gln Ala Gly Arg Leu Ala Gly
 3780 3785 3790

Phe Val Ala Gly Asp Ala Ser Leu Ala Gly Val Ala Arg Ala Leu Val
 3795 3800 3805

Thr Asn Arg Ala Ala Leu Thr Glu Arg Ala Val Met Val Val Gly Ser
 3810 3815 3820

Arg Glu Glu Ala Val Thr Asn Leu Glu Ala Leu Ala Arg Gly Glu Asp
 3825 3830 3835 3840

Pro Ala Ala Val Val Thr Gly Arg Ala Gly Ser Pro Gly Lys Leu Val
 3845 3850 3855

Trp Val Phe Pro Gly Gln Gly Ser Gln Trp Ile Gly Met Gly Arg Glu
 3860 3865 3870

Leu Leu Asp Ser Ser Pro Val Phe Ala Glu Arg Val Ala Glu Cys Ala
 3875 3880 3885

Ala Ala Leu Glu Pro Trp Ile Asp Trp Ser Leu Leu Asp Val Leu Arg
 3890 3895 3900

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Gly Glu Ser Asp Leu Leu Asp Arg Val Asp Val Val Gln Pro Ala Ser			
3905	3910	3915	3920
Phe Ala Met Met Val Gly Leu Ala Ala Val Trp Gln Ser Val Gly Val			
	3925	3930	3935
Arg Pro Asp Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala			
3940	3945		3950
Cys Val Ser Gly Ala Leu Ser Leu Gln Asp Ala Ala Lys Val Val Ala			
3955	3960		3965
Leu Arg Ser Gln Ala Ile Ala Thr Arg Leu Ala Gly Arg Gly Gly Met			
3970	3975		3980
Ala Ser Val Ala Leu Ser Glu Glu Asp Ala Thr Ala Trp Leu Ala Pro			
3985	3990	3995	4000
Trp Ala Asp Arg Val Gln Val Ala Ala Val Asn Ser Pro Ala Ser Val			
	4005	4010	4015
Val Ile Ala Gly Glu Ala Gln Ala Leu Asp Glu Val Val Asp Ala Leu			
	4020	4025	4030
Ser Gly Gln Glu Val Arg Val Arg Arg Val Ala Val Asp Tyr Gly Ser			
4035	4040		4045
His Thr Asn Gln Val Glu Ala Ile Glu Asp Leu Leu Ala Glu Thr Leu			
4050	4055		4060
Ala Gly Ile Glu Ala Gln Ala Pro Lys Val Pro Phe Tyr Ser Thr Leu			
4065	4070	4075	4080
Ile Gly Asp Trp Ile Arg Asp Ala Gly Ile Val Asp Gly Gly Tyr Trp			
	4085	4090	4095
Tyr Arg Asn Leu Arg Asn Gln Val Gly Phe Gly Pro Ala Val Ala Glu			

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4100	4105	4110
Leu Val Arg Gln Gly His Gly Val Phe Val Glu Val Ser Ala His Pro		
4115	4120	4125
Val Leu Val Gln Pro Leu Ser Glu Leu Ser Asp Asp Ala Val Val Thr		
4130	4135	4140
Gly Ser Leu Arg Arg Glu Asp Gly Gly Leu Arg Arg Leu Leu Thr Ser		
4145	4150	4155
Met Ala Glu Leu Tyr Val Gln Gly Val Pro Leu Asp Trp Thr Ala Val		
4165	4170	4175
Leu Pro Arg Thr Gly Arg Val Asp Leu Pro Lys Tyr Ala Phe Asp His		
4180	4185	4190
Arg His Tyr Trp Leu Arg Pro Ala Glu Ser Ala Thr Asp Ala Ala Ser		
4195	4200	4205
Leu Gly Gln Ala Ala Ala Asp His Pro Leu Leu Gly Ala Val Val Glu		
4210	4215	4220
Leu Pro Gln Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Val Arg		
4225	4230	4235
Thr His Pro Trp Leu Ala Asp His Ala Val Gly Gly Val Val Ile Leu		
4245	4250	4255
Pro Gly Ser Gly Leu Ala Glu Leu Ala Val Arg Ala Gly Asp Glu Ala		
4260	4265	4270
Gly Cys Thr Ala Leu Asp Glu Leu Ile Ile Glu Ala Pro Leu Val Val		
4275	4280	4285
Pro Ala Gln Gly Ala Val Arg Val Gln Val Ala Leu Ser Gly Pro Asp		
4290	4295	4300

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Glu Thr Gly Ser Arg Thr Val Asp Leu Tyr Ser Gln Arg Asp Gly Gly
 4305 4310 4315 4320

Ala Gly Thr Trp Thr Arg His Ala Thr Gly Val Leu Ser Thr Ala Pro
 4325 4330 4335

Ala Gln Glu Pro Glu Phe Asp Phe His Ala Trp Pro Pro Ala Asp Ala
 4340 4345 4350

Glu Arg Ile Asp Val Glu Thr Phe Tyr Thr Asp Leu Ala Glu Arg Gly
 4355 4360 4365

Tyr Gly Tyr Gly Pro Ala Phe Gln Gly Leu Gln Ala Val Trp Arg Arg
 4370 4375 4380

Asp Gly Asp Val Phe Ala Glu Val Ala Leu Pro Glu Asp Leu Arg Lys
 4385 4390 4395 4400

Asp Ala Gly Arg Phe Gly Val His Pro Ala Leu Leu Asp Ala Ala Leu
 4405 4410 4415

Gln Ala Ala Thr Ala Val Gly Gly Asp Glu Pro Gly Gln Pro Val Leu
 4420 4425 4430

Ala Phe Ala Trp Asn Gly Leu Val Leu His Ala Ala Gly Ala Ser Ala
 4435 4440 4445

Leu Arg Val Arg Leu Ala Pro Ser Gly Pro Asp Thr Leu Ser Val Ala
 4450 4455 4460

Ala Ala Asp Glu Thr Gly Gly Leu Val Leu Thr Met Glu Ser Leu Val
 4465 4470 4475 4480

Ser Arg Pro Val Ser Ala Glu Gln Leu Gly Ala Ala Ala Asp Ala Gly
 4485 4490 4495

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His Asp Ala Met Phe Arg Val Asp Trp Thr Glu Leu Pro Ala Val Pro
 4500 4505 4510

Arg Ala Glu Leu Pro Pro Trp Val Arg Ile Asp Thr Ala Asp Asp Val
 4515 4520 4525

Ala Ala Leu Ala Glu Lys Ala Asp Ala Pro Pro Val Val Val Trp Glu
 4530 4535 4540

Ala Ala Gly Gly Asp Pro Ala Leu Ala Val Ser Ser Arg Val Leu Glu
 4545 4550 4555 4560

Ile Met Gln Ala Trp Leu Ala Ala Pro Ala Phe Glu Glu Ala Arg Leu
 4565 4570 4575

Val Val Thr Thr Arg Gly Ala Val Pro Ala Gly Gly Asp His Thr Leu
 4580 4585 4590

Thr Asp Pro Ala Ala Ala Ala Val Trp Gly Leu Val Arg Ser Ala Gln
 4595 4600 4605

Ala Glu His Pro Asp Arg Val Val Leu Leu Asp Thr Asp Gly Glu Val
 4610 4615 4620

Pro Leu Gly Ala Val Leu Ala Ser Gly Glu Pro Gln Leu Ala Val Arg
 4625 4630 4635 4640

Gly Thr Thr Phe Phe Val Pro Arg Leu Ala Arg Ala Thr Arg Leu Ser
 4645 4650 4655

Asp Ala Pro Pro Ala Phe Asp Pro Asp Gly Thr Val Leu Val Ser Gly
 4660 4665 4670

Ala Gly Ser Leu Gly Thr Leu Val Ala Arg His Leu Val Thr Arg His
 4675 4680 4685

Gly Val Arg Arg Val Val Leu Ala Ser Arg Gln Gly Arg Asp Ala Glu

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4690	4695	4700	
Gly Ala Gln Asp Leu Ile Thr Glu Leu Thr Gly Glu Gly Ala Asp Val			
4705	4710	4715	4720
Ser Phe Val Ala Cys Asp Val Ser Asp Arg Asp Gln Val Ala Ala Leu			
	4725	4730	4735
Leu Ala Gly Leu Pro Asp Leu Thr Gly Val Val His Thr Ala Gly Val			
	4740	4745	4750
Phe Glu Asp Gly Val Ile Glu Ala Leu Thr Pro Asp Gln Leu Ala Asn			
	4755	4760	4765
Val Tyr Ala Ala Lys Val Thr Ala Ala Met His Leu Asp Glu Leu Thr			
	4770	4775	4780
Arg Asp Arg Asp Leu Gly Ala Phe Val Val Phe Ser Ser Val Ala Gly			
4785	4790	4795	4800
Val Met Gly Gly Gly Gly Gln Gly Pro Tyr Ala Ala Ala Asn Ala Phe			
	4805	4810	4815
Leu Asp Ala Ala Met Ala Ser Arg Gln Ala Ala Gly Leu Pro Gly Leu			
	4820	4825	4830
Ser Leu Ala Trp Gly Leu Trp Glu Arg Ser Ser Gly Met Ala Ala His			
	4835	4840	4845
Leu Ser Glu Val Asp His Ala Arg Ala Ser Arg Asn Gly Val Leu Glu			
	4850	4855	4860
Leu Thr Arg Ala Glu Gly Leu Ala Leu Phe Asp Leu Gly Leu Arg Met			
4865	4870	4875	4880
Ala Glu Ser Leu Leu Val Pro Ile Lys Leu Asp Leu Ala Ala Met Arg			
	4885	4890	4895

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Ala Ser Thr Val Pro Val Leu Phe Arg Gly Leu Val Arg Pro Ser Arg
 4900 4905 4910

Thr Gln Ala Arg Thr Ala Ser Thr Val Asp Arg Gly Leu Ala Gly Arg
 4915 4920 4925

Leu Ala Gly Leu Pro Val Ala Glu Arg Ala Ala Val Leu Val Asp Leu
 4930 4935 4940

Val Arg Gly Gln Val Ala Val Val Leu Gly Tyr Asp Gly Pro Glu Ala
 4945 4950 4955 4960

Val Arg Pro Asp Thr Ala Phe Lys Asp Thr Gly Phe Asp Ser Leu Thr
 4965 4970 4975

Ser Val Glu Leu Arg Asn Arg Leu Arg Glu Ala Thr Gly Leu Lys Leu
 4980 4985 4990

Pro Ala Thr Leu Val Phe Asp Tyr Pro Asn Pro Leu Ala Val Ala Arg
 4995 5000 5005

Tyr Leu Gly Ala Arg Leu Val Pro Asp Gly Thr Ala Asn Gly Asn Gly
 5010 5015 5020

Asn Gly Asn Gly His Ser Glu Asp Asp Arg Leu Arg His Ala Leu Ala
 5025 5030 5035 5040

Ala Ile Ala Ala Glu Asp Ala Gly Glu Glu Arg Ser Ile Ala Asp Leu
 5045 5050 5055

Gly Val Asp Asp Leu Val Gln Leu Ala Phe Gly Asp Glu
 5060 5065

(2) INFORMATION FOR SEQ ID NO: 6:

(1) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1721 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Ala	Cys	Arg	Leu	Pro	Gly	Gly	Val	Thr	Gly	Pro	Gly	Asp	Leu	Trp
1				5					10					15	
Arg	Leu	Val	Ala	Glu	Gly	Gly	Asp	Ala	Val	Ser	Gly	Phe	Pro	Thr	Asp
				20				25					30		
Arg	Cys	Trp	Asp	Leu	Asp	Thr	Leu	Phe	Asp	Pro	Asp	Pro	Asp	His	Ala
				35			40					45			
Gly	Thr	Ser	Tyr	Thr	Asp	Gln	Gly	Gly	Phe	Leu	His	Asp	Ala	Ala	Leu
				50			55					60			
Phe	Asp	Pro	Gly	Phe	Phe	Gly	Ile	Ser	Pro	Arg	Glu	Ala	Leu	Ala	Met
65					70					75				80	
Asp	Pro	Gln	Gln	Arg	Leu	Leu	Leu	Glu	Ala	Ser	Trp	Glu	Ala	Leu	Glu
				85					90					95	
Gly	Val	Gly	Leu	Asp	Pro	Ala	Ser	Leu	Gln	Gly	Thr	Asp	Val	Gly	Val
				100					105				110		
Phe	Thr	Gly	Ala	Gly	Gly	Ser	Gly	Tyr	Gly	Gly	Gly	Leu	Thr	Gly	Pro
				115				120					125		
Glu	Met	Gln	Ser	Phe	Ala	Gly	Thr	Gly	Leu	Ala	Ser	Ser	Val	Ala	Ser

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130	135	140
Gly Arg Val Ser Tyr Val Phe Gly Phe Glu Gly Pro Ala Val Thr Ile		
145	150	155 160
Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Met His Leu Ala Ala Gln		
165	170	175
Ala Leu Arg Gln Gly Asp Cys Ser Met Ala Leu Ala Gly Gly Ala Met		
180	185	190
Val Met Ser Gly Pro Asp Ser Phe Val Val Phe Ser Arg Gln Arg Gly		
195	200	205
Leu Ala Thr Asp Gly Arg Cys Lys Ala Phe Ala Ser Gly Ala Asp Gly		
210	215	220
Met Val Leu Ala Glu Gly Ile Ser Val Val Val Leu Glu Arg Leu Ser		
225	230	235 240
Val Ala Arg Glu Arg Gly His Arg Val Leu Ala Val Leu Arg Gly Ser		
245	250	255
Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly		
260	265	270
Pro Ser Gln Gln Arg Val Ile Arg Ala Ala Leu Ala Asn Ala Gly Ile		
275	280	285
Gly Pro Ser Asp Val Asp Leu Val Glu Ala His Gly Thr Gly Thr Ser		
290	295	300
Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Gln		
305	310	315 320
Asp Arg Glu Thr Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly		
325	330	335

His Thr Gln Ala Ala Ala Gly Val Ala Ser Val Ile Lys Val Val Gln
340 345 350

Ala Leu Arg His Gly Val Met Pro Pro Thr Leu His Val Asp Glu Pro
355 360 365

Ser Ser Gln Val Asp Trp Ser Glu Gly Ala Val Glu Leu Leu Thr Gly
370 375 380

Ser Arg Asp Trp Pro Arg Gly Asp Arg Pro Arg Arg Ala Gly Val Ser
385 390 395 400

Ser Phe Gly Val Ser Gly Thr Asn Val His Leu Ile Ile Glu Glu Ala
405 410 415

Pro Glu Glu Pro Ala Ala Ala Val Pro Thr Ser Ala Asp Val Val Pro
420 425 430

Leu Val Val Ser Ala Arg Ser Thr Gly Ser Leu Ala Gly Gln Ala Asp
435 440 445

Arg Leu Thr Glu Val Asp Val Pro Leu Gly His Leu Ala Gly Ala Leu
450 455 460

Val Ala Gly Arg Ala Val Leu Glu Glu Arg Ala Val Val Val Ala Gly
465 470 475 480

Ser Ala Glu Glu Ala Arg Ala Gly Leu Gly Ala Leu Ala Arg Gly Glu
485 490 495

Ala Ala Pro Gly Val Val Thr Gly Thr Ala Gly Lys Pro Gly Lys Val
500 505 510

Val Trp Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Arg
515 520 525

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Glu Leu Leu Asp Ala Ser Pro Val Phe Ala Glu Arg Ile Lys Glu Cys
 530 535 540

Ala Ala Ala Leu Asp Gln Trp Thr Asp Trp Ser Leu Leu Asp Val Leu
 545 550 555 560

Arg Gly Asp Gly Asp Leu Asp Ser Val Glu Val Leu Gln Pro Ala Cys
 565 570 575

Phe Ala Val Met Val Gly Leu Ala Ala Val Trp Glu Ser Ala Gly Val
 580 585 590

Arg Pro Asp Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala
 595 600 605

Cys Val Ser Gly Ala Leu Thr Leu Asp Asp Ala Ala Lys Val Val Ala
 610 615 620

Leu Arg Ser Gln Ala Ile Ala Ala Arg Leu Ser Gly Arg Gly Gly Met
 625 630 635 640

Ala Ser Val Ala Leu Ser Glu Asp Glu Ala Asn Ala Arg Leu Gly Leu
 645 650 655

Trp Asp Gly Arg Ile Glu Val Ala Ala Val Asn Gly Pro Ala Ser Val
 660 665 670

Val Ile Ala Gly Asp Ala Gln Ala Leu Asp Glu Ala Leu Glu Val Leu
 675 680 685

Ala Gly Asp Gly Val Arg Val Arg Gln Val Ala Val Asp Tyr Ala Ser
 690 695 700

His Thr Arg His Val Glu Asp Ile Arg Asp Thr Leu Ala Glu Thr Leu
 705 710 715 720

Ala Gly Ile Thr Ala Gln Ala Pro Asp Val Pro Phe Arg Ser Thr Val

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725	730	735
Thr Gly Gly Trp Val Arg Asp Ala Asp Val Leu Asp Gly Gly Tyr Trp		
740	745	750
Tyr Arg Asn Leu Arg Asn Gln Val Arg Phe Gly Pro Ala Val Ala Glu		
755	760	765
Leu Leu Glu Gln Gly His Gly Val Phe Val Glu Val Ser Ala His Pro		
770	775	780
Val Leu Val Gln Pro Ile Ser Glu Leu Thr Asp Ala Val Val Thr Gly		
785	790	800
Thr Leu Arg Arg Asp Asp Gly Gly Leu Arg Arg Leu Leu Thr Ser Met		
805	810	815
Ala Glu Leu Phe Val Arg Gly Val Arg Val Asp Trp Ala Thr Leu Val		
820	825	830
Pro Pro Ala Arg Val Asp Leu Pro Thr Tyr Ala Phe Asp His Gln His		
835	840	845
Phe Trp Leu Arg Pro Ala Ala Gln Ala Asp Ala Val Ser Leu Gly Gln		
850	855	860
Ala Ala Ala Glu His Pro Leu Leu Gly Ala Val Val Arg Leu Pro Gln		
865	870	875
Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Leu Arg Thr His Pro		
885	890	895
Trp Leu Ala Asp His Thr Ile Gly Gly Val Val Leu Phe Pro Gly Thr		
900	905	910
Gly Leu Val Glu Leu Ala Val Arg Ala Gly Asp Glu Ala Gly Cys Pro		
915	920	925

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Val Leu Asp Glu Leu Val Thr Glu Ala Pro Leu Val Val Pro Gly Gln
 930 935 940

Gly Gly Val Asn Val Gln Val Thr Val Ser Gly Pro Asp Gln Asn Gly
 945 950 955 960

Leu Arg Thr Val Asp Ile His Ser Gln Arg Asp Asp Val Trp Thr Arg
 965 970 975

His Ala Thr Gly Thr Val Ser Ala Thr Pro Ala Ser Ser Pro Gly Phe
 980 985 990

Asp Phe Thr Ala Trp Pro Pro Pro Asp Gly Gln Arg Val Glu Ile Gly
 995 1000 1005

Asp Phe Tyr Ala Asp Leu Ala Glu Arg Gly Tyr Ala Tyr Gly Pro Leu
 1010 1015 1020

Phe Gln Gly Val Arg Ala Val Trp Gln Arg Gly Glu Asp Val Phe Ala
 1025 1030 1035 1040

Glu Val Ala Leu Pro Glu Asp Arg Arg Glu Asp Ala Ala Arg Phe Gly
 1045 1050 1055

Leu His Pro Ala Leu Leu Asp Ala Ala Leu Gln Thr Gly Thr Ile Ala
 1060 1065 1070

Ala Ala Ala Ser Gly Gln Pro Gly Lys Ser Val Met Pro Phe Ser Trp
 1075 1080 1085

Asn Arg Leu Ala Leu His Ala Val Gly Ala Ala Gly Leu Arg Val Arg
 1090 1095 1100

Val Ala Pro Gly Gly Pro Asp Ala Leu Thr Val Glu Ala Ala Asp Glu
 1105 1110 1115 1120

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Thr Gly Ala Pro Val Leu Thr Met Asp Ser Leu Ile Leu Arg Glu Val
 1125 1130 1135

Ala Leu Asp Gln Leu Asp Thr Ala Arg Ala Gly Ser Leu Tyr Arg Val
 1140 1145 1150

Asp Trp Thr Pro Leu Pro Thr Val Asp Ser Ala Val Pro Ala Gly Arg
 1155 1160 1165

Ala Glu Val Leu Glu Ala Phe Gly Glu Glu Pro Leu Asp Leu Thr Gly
 1170 1175 1180

Arg Val Leu Ala Ala Leu Gln Ala Trp Leu Ser Asp Ala Ala Glu Glu
 1185 1190 1195 1200

Ala Arg Leu Val Val Val Thr Arg Gly Ala Val Pro Ala Gly Asp Gly
 1205 1210 1215

Val Val Ser Asp Pro Ala Gly Ala Ala Val Trp Gly Leu Val Arg Ala
 1220 1225 1230

Ala Gln Ala Glu Asn Pro Asp Arg Phe Val Leu Leu Asp Thr Asp Gly
 1235 1240 1245

Glu Val Pro Leu Glu Ala Val Leu Ala Thr Gly Glu Pro Gln Leu Ala
 1250 1255 1260

Leu Arg Gly Thr Thr Phe Ser Val Pro Arg Leu Ala Arg Val Thr Glu
 1265 1270 1275 1280

Pro Ala Glu Ala Pro Leu Thr Phe Arg Pro Asp Gly Thr Val Leu Val
 1285 1290 1295

Ser Gly Ala Gly Thr Leu Gly Ala Leu Ala Ala Arg Asp Leu Val Thr
 1300 1305 1310

Arg His Gly Val Arg Arg Leu Val Leu Ala Ser Arg Arg Gly Arg Ala

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1315	1320	1325
Ala Glu Gly Ile Asp Asp Leu Val Ala Glu Leu Thr Gly His Gly Ala		
1330	1335	1340
Glu Val Thr Val Ala Ala Cys Asp Val Ser Asp Arg Asp Gln Val Ala		
1345	1350	1355
		1360
Ala Leu Leu Lys Glu His Ala Leu Thr Ala Val Val His Thr Ala Gly		
1365	1370	1375
Val Phe Asp Ala Gly Val Thr Gly Ala Leu Thr Arg Glu Arg Leu Ala		
1380	1385	1390
Lys Val Phe Ala Pro Lys Val Asp Ala Ala Asn His Leu Asp Glu Leu		
1395	1400	1405
Thr Arg Asp Leu Asp Leu Asp Ala Phe Ile Val Tyr Ser Ser Ala Ser		
1410	1415	1420
Ser Ile Phe Met Gly Ala Gly Ser Gly Gly Tyr Ala Ala Ala Asn Ala		
1425	1430	1435
		1440
Tyr Leu Asp Gly Leu Met Ala Ala Arg Arg Ala Ala Gly Leu Pro Gly		
1445	1450	1455
Leu Ser Leu Ala Trp Gly Pro Trp Glu Gln Leu Thr Gly Met Ala Asp		
1460	1465	1470
Thr Ile Asp Asp Leu Thr Leu Ala Arg Met Ser Arg Arg Glu Gly Arg		
1475	1480	1485
Gly Gly Val Arg Ala Leu Gly Ser Ala Asp Gly Met Glu Leu Phe Asp		
1490	1495	1500
Ala Ala Leu Ala Ala Gly Gln Ala Leu Leu Val Pro Ile Glu Leu Asp		
1505	1510	1515
		1520

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Leu Arg Glu Val Arg Ala Asp Ala Ala Gly Gly Gly Thr Val Pro His
 1525 1530 1535

Leu Leu Arg Gly Leu Val Arg Ala Gly Arg Gln Ala Ala Arg Thr Ala
 1540 1545 1550

Ala Thr Glu Asp Gly Gly Leu Glu Arg Arg Leu Ala Gly Leu Thr Val
 1555 1560 1565

Ala Glu Gln Glu Ala Leu Leu Leu Asp Leu Val Arg Gly Gln Val Ala
 1570 1575 1580

Val Val Leu Gly His Ala Asp Ser Ser Gly Val Arg Ala Asp Ala Ala
 1585 1590 1595 1600

Phe Lys Asp Ala Gly Phe Asp Ser Leu Thr Ser Val Glu Leu Arg Asn
 1605 1610 1615

Arg Leu Arg Glu Thr Thr Gly Leu Lys Leu Pro Ala Thr Leu Val Phe
 1620 1625 1630

Asp His Pro Asn Pro Leu Ala Leu Ala Arg His Leu Arg Ala Glu Leu
 1635 1640 1645

Ala Val Asp Glu Ala Ser Pro Ala Asp Ala Val Leu Ala Gly Leu Ala
 1650 1655 1660

Gly Leu Glu Ala Ala Ile Ala Ala Ala Gly Ala Pro Asp Gly Asp Arg
 1665 1670 1675 1680

Ile Thr Ala Arg Leu Arg Glu Leu Leu Lys Ala Ala Glu Ala Ala Glu
 1685 1690 1695

Ala Arg Pro Gly Thr Ser Gly Asp Leu Asp Thr Ala Ser Asp Glu Glu
 1700 1705 1710

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Leu Phe Ala Leu Val Asp Gly Leu Asp
 1715 1720

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1688 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ala Cys Arg Tyr Pro Gly Gly Val Ser Ser Pro Glu Asp Leu Trp
 1 5 10 15

Arg Leu Val Ala Glu Gly Thr Asp Ala Val Ser Ala Phe Pro Gly Asp
 20 25 30

Arg Gly Trp Asp Val Asp Gly Leu Val Asp Pro Asp Pro Asp Arg Pro
 35 40 45

Gly Thr Thr Tyr Thr Asp Gln Gly Gly Phe Leu His Glu Ala Gly Leu
 50 55 60

Phe Asp Ala Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Val Ala Met
 65 70 75 80

Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Ile Glu
 85 90 95

Arg Thr Gly Thr Asp Pro Leu Ser Leu Lys Gly Ser Asp Ile Gly Val

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100	105	110
Phe Thr Gly Val Ala Ser Met Gly Tyr Gly Ala Gly Gly Gly Val Val		
115	120	125
Ala Pro Glu Leu Glu Gly Phe Val Gly Thr Gly Ala Ala Pro Cys Ile		
130	135	140
Ala Ser Gly Arg Val Ser Tyr Val Leu Gly Phe Glu Gly Pro Ala Val		
145	150	155
		160
Thr Val Asp Thr Gly Cys Ser Ser Ser Leu Val Ala Met His Leu Ala		
165	170	175
Ala Gln Ala Leu Arg Arg Gly Glu Cys Ser Met Ala Leu Ala Gly Gly		
180	185	190
Ala Met Val Met Ala Gln Pro Gly Ser Phe Val Ser Phe Ser Arg Gln		
195	200	205
Arg Gly Leu Ala Leu Asp Gly Arg Cys Lys Ala Phe Ser Asp Ser Ala		
210	215	220
Asp Gly Met Gly Leu Ala Glu Gly Val Gly Val Ile Ala Leu Glu Arg		
225	230	235
		240
Leu Ser Val Ala Arg Glu Arg Gly His Arg Val Leu Ala Val Leu Arg		
245	250	255
Gly Ile Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro		
260	265	270
Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Ala Ala Leu Ala Glu Ala		
275	280	285
Gly Leu Ser Pro Ser Asp Val Asp Ala Val Glu Gly His Gly Thr Gly		
290	295	300

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Thr Thr Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr			
305	310	315	320
Gly Lys Gly Arg Asp Pro Glu Lys Pro Leu Trp Leu Gly Ser Val Lys			
	325	330	335
Ser Asn Leu Gly His Thr Gln Ala Ala Ala Gly Val Ala Ser Val Ile			
	340	345	350
Lys Met Val Gln Ala Leu Arg His Gly Val Leu Pro Pro Thr Leu His			
	355	360	365
Val Asp Arg Pro Ser Thr Glu Val Asp Trp Ser Ala Gly Ala Val Ser			
	370	375	380
Leu Leu Thr Glu Ala Arg Glu Trp Pro Arg Glu Gly Arg Pro Arg Arg			
385	390	395	400
Ala Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Leu Ile			
	405	410	415
Leu Glu Glu Ala Pro Glu Glu Glu Pro Pro Val Ala Glu Ala Pro Ser			
	420	425	430
Ala Gly Val Val Pro Val Val Val Ser Ala Arg Gly Ala Leu Ala Gly			
	435	440	445
Gln Ala Gly Arg Leu Ala Ala Phe Leu Glu Ala Ser Asp Glu Pro Leu			
	450	455	460
Val Thr Val Ala Gly Ala Leu Ile Cys Gly Arg Ser Arg Phe Gly Asp			
465	470	475	480
Arg Ala Val Val Val Ala Gly Thr Arg Ala Glu Ala Thr Ala Gly Leu			
	485	490	495

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Ala Ala Leu Ala Arg Gly Glu Ser Ala Ala Asp Val Val Thr Gly Thr
 500 505 510

Val Ala Ala Ser Gly Val Pro Gly Lys Leu Val Trp Val Phe Pro Gly
 515 520 525

Gln Gly Ser Gln Trp Val Gly Met Gly Arg Glu Leu Leu Glu Ala Ser
 530 535 540

Pro Val Phe Ala Ala Arg Ile Ala Glu Cys Ala Ala Ala Leu Glu Pro
 545 550 555 560

Trp Ile Asp Trp Ser Leu Leu Asp Val Leu Arg Gly Glu Gly Asp Leu
 565 570 575

Asp Arg Val Asp Val Val Gln Pro Ala Ser Phe Ala Val Met Val Gly
 580 585 590

Leu Ala Ala Val Trp Ser Ser Val Gly Val Val Pro Asp Ala Val Leu
 595 600 605

Gly His Ser Gln Gly Glu Ile Ala Ala Ala Cys Val Ser Gly Ala Leu
 610 615 620

Ser Leu Gln Asp Ala Ala Lys Val Val Ala Leu Arg Ser Gln Ala Ile
 625 630 635 640

Ala Ala Lys Leu Ala Gly Arg Gly Gly Met Ala Ser Val Ala Leu Ser
 645 650 655

Glu Glu Asp Ala Val Ala Arg Leu Arg His Trp Ala Asp Arg Val Glu
 660 665 670

Val Ala Ala Val Asn Ser Pro Ser Ser Val Val Ile Ala Gly Asp Ala
 675 680 685

Glu Ala Leu Asp Gln Ala Leu Glu Ala Leu Thr Gly Gln Asp Ile Arg

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690	695	700
Val Arg Arg Val Ala Val Asp Tyr Ala Ser His Thr Arg His Val Glu		
705	710	715 720
Asp Ile Gln Glu Pro Leu Ala Glu Ala Leu Ala Gly Ile Glu Ala His		
725	730	735
Ala Pro Thr Leu Pro Phe Phe Ser Thr Leu Thr Gly Asp Trp Ile Arg		
740	745	750
Glu Ala Gly Val Val Asp Gly Gly Tyr Trp Tyr Arg Asn Leu Arg Asn		
755	760	765
Gln Val Gly Phe Gly Pro Ala Val Ala Glu Leu Leu Gly Leu Gly His		
770	775	780
Arg Val Phe Val Glu Val Ser Ala His Pro Val Leu Val Gln Ala Ile		
785	790	795 800
Ser Ala Ile Ala Asp Asp Thr Asp Ala Val Val Thr Gly Ser Leu Arg		
805	810	815
Arg Glu Glu Gly Gly Leu Arg Arg Leu Leu Thr Ser Met Ala Glu Leu		
820	825	830
Phe Val Arg Gly Val Asp Val Asp Trp Ala Thr Met Val Pro Pro Ala		
835	840	845
Arg Val Asp Leu Pro Thr Tyr Ala Phe Asp His Gln His Tyr Trp Leu		
850	855	860
Arg Tyr Val Glu Thr Ala Thr Asp Ala Ala Gly Pro Val Val Arg Leu		
865	870	875 880
Pro Gln Thr Gly Gly Leu Val Phe Thr Thr Glu Trp Ser Leu Lys Ser		
885	890	895

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Gln Pro Trp Leu Ala Glu His Thr Leu Glu Asp Leu Val Val Val Pro
 900 905 910

Gly Ala Ala Leu Val Glu Leu Ala Val Arg Ala Gly Asp Glu Ala Gly
 915 920 925

Thr Pro Val Leu Asp Glu Leu Val Ile Glu Thr Pro Leu Val Val Pro
 930 935 940

Glu Arg Gly Ala Ile Arg Val Gln Val Thr Val Ser Gly Pro Asp Asp
 945 950 955 960

Gly Thr Arg Thr Leu Glu Val His Ser Gln Pro Glu Asp Ala Thr Asp
 965 970 975

Glu Trp Thr Arg His Ala Thr Gly Thr Leu Ser Ala Thr Pro Asp Glu
 980 985 990

Ser Ser Gly Phe Asp Phe Thr Ala Trp Pro Pro Pro Gly Ala Arg Gln
 995 1000 1005

Leu Asp Gly Val Pro Ala Ile Trp Arg Ala Gly Asp Glu Ile Phe Ala
 1010 1015 1020

Glu Val Ser Leu Pro Asp Asp Ala Asp Ala Glu Ala Phe Gly Ile His
 1025 1030 1035 1040

Pro Ala Leu Leu Asp Ala Ala Leu His Pro Ala Leu Pro Gly Asp Asp
 1045 1050 1055

Gly Leu Thr Gln Pro Met Glu Trp Arg Gly Leu Thr Leu His Ala Ala
 1060 1065 1070

Gly Ala Ser Thr Leu Arg Val Arg Leu Val Pro Gly Gly Phe Leu Glu
 1075 1080 1085

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Ala Ala Asp Gly Ala Gly Ser Leu Val Val Thr Ala Lys Glu Val Ala
 1090 1095 1100

Leu Arg Pro Val Thr Ile Ala Arg Ser Arg Thr Thr Thr Arg Asp Ser
 1105 1110 1115 1120

Leu Phe Gln Leu Asn Trp Ile Glu Leu Pro Glu Ser Gly Val Val Ala
 1125 1130 1135

Ala Ala Asp Asp Thr Glu Val Leu Glu Val Pro Ala Gly Asp Ser Pro
 1140 1145 1150

Leu Ala Ala Thr Ser Arg Val Leu Glu Arg Leu Gln Thr Trp Leu Thr
 1155 1160 1165

Glu Pro Glu Ala Glu Gln Leu Val Val Val Thr Arg Gly Ala Val Pro
 1170 1175 1180

Ala Gly Asp Thr Pro Val Thr Asp Pro Ala Ala Ala Val Trp Gly
 1185 1190 1195 1200

Leu Val Arg Ser Ala Gln Ala Glu Asn Pro Asp Arg Ile Val Leu Leu
 1205 1210 1215

Asp Thr Asp Gly Glu Val Pro Leu Gly Ala Val Leu Ala Gly Gly Glu
 1220 1225 1230

Pro Gln Val Ala Val Arg Gly Thr Ala Leu Tyr Val Pro Arg Leu Ala
 1235 1240 1245

Arg Ala Asp Ala Ala Pro Val Ser Gly Leu His Gly Thr Val Leu Val
 1250 1255 1260

Ser Gly Ala Gly Val Leu Gly Glu Ile Val Ala Arg His Leu Val Thr
 1265 1270 1275 1280

Arg His Gly Val Arg Lys Leu Val Leu Ala Ser Arg Arg Gly Leu Asp

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1285	1290	1295
Ala Asp Gly Ala Lys Asp Leu Val Thr Asp Leu Thr Gly Glu Gly Ala		
1300	1305	1310
Asp Val Ser Val Val Ala Cys Asp Leu Ala Asp Arg Asn Gln Val Ala		
1315	1320	1325
Ala Leu Leu Ala Asp His Arg Pro Ala Ser Val Ile His Thr Ala Gly		
1330	1335	1340
Val Leu Asp Asp Gly Val Ile Gly Thr Leu Thr Pro Glu Arg Leu Ala		
1345	1350	1355
Lys Val Phe Ala Pro Lys Val Asp Ala Val Arg His Leu Asp Glu Leu		
1365	1370	1375
Thr Arg Asp Leu Asp Leu Asp Ala Phe Val Val Phe Ser Ser Gly Ser		
1380	1385	1390
Gly Val Phe Gly Ser Pro Gly Gln Gly Asn Tyr Ala Ala Ala Asn Ala		
1395	1400	1405
Phe Leu Asp Ala Ala Met Ala Ser Arg Arg Ala Ala Gly Leu Pro Gly		
1410	1415	1420
Leu Ser Leu Ala Trp Gly Leu Trp Glu Gln Ala Thr Gly Met Thr Ala		
1425	1430	1435
His Leu Gly Gly Thr Asp Gln Ala Arg Met Ser Arg Gly Gly Val Arg		
1445	1450	1455
Pro Ile Thr Ala Glu Glu Gly Met Ala Leu Phe Asp Thr Ala Leu Gly		
1460	1465	1470
Ala Gln Pro Ala Leu Leu Val Pro Val Lys Leu Asp Leu Arg Glu Val		
1475	1480	1485

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Arg Ala Gly Gly Ala Val Pro His Leu Leu Arg Gly Leu Val Arg Ala
 1490 1495 1500

Gly Arg Arg Gln Ala Gln Ala Ala Ser Thr Val Asp Asn Gln Leu Leu
 1505 1510 1515 1520

Gly Arg Leu Ala Gly Leu Gly Ala Pro Glu Gln Glu Ala Leu Leu Val
 1525 1530 1535

Asp Leu Val Arg Gly Gln Val Ala Ala Val Leu Gly His Ala Gly Pro
 1540 1545 1550

Asp Ala Val Arg Ala Asp Thr Ala Phe Lys Asp Ala Gly Phe Asp Ser
 1555 1560 1565

Leu Thr Ser Val Asp Leu Arg Asn Arg Leu Arg Glu Ser Thr Gly Leu
 1570 1575 1580

Lys Leu Pro Ala Thr Leu Ala Phe Asp Tyr Pro Thr Pro Leu Val Leu
 1585 1590 1595 1600

Ala Arg His Leu Arg Asp Glu Leu Gly Ala Gly Asp Asp Ala Leu Ser
 1605 1610 1615

Val Val His Ala Arg Leu Glu Asp Val Glu Ala Leu Leu Gly Gly Leu
 1620 1625 1630

Arg Leu Asp Glu Ser Thr Lys Thr Gly Leu Thr Leu Arg Leu Gln Gly
 1635 1640 1645

Leu Val Ala Arg Cys Asn Gly Val Asn Asp Gln Thr Gly Gly Glu Thr
 1650 1655 1660

Leu Ala Asp Arg Leu Glu Ala Ala Ser Ala Asp Glu Val Leu Asp Phe
 1665 1670 1675 1680

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Ile Asp Glu Glu Leu Gly Leu Thr
1685

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3413 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Ala	Thr	Asp	Glu	Lys	Leu	Leu	Lys	Tyr	Leu	Lys	Arg	Val	Thr	Ala
1					5				10					15	
Glu	Leu	His	Ser	Leu	Arg	Lys	Gln	Gly	Ala	Arg	His	Ala	Asp	Glu	Pro
				20				25					30		
Leu	Ala	Val	Val	Gly	Met	Ala	Cys	Arg	Phe	Pro	Gly	Gly	Val	Ser	Ser
				35				40					45		
Pro	Glu	Asp	Leu	Trp	Gln	Leu	Val	Ala	Gly	Gly	Val	Asp	Ala	Leu	Ser
				50			55					60			
Asp	Phe	Pro	Asp	Asp	Arg	Gly	Trp	Glu	Leu	Asp	Gly	Leu	Phe	Asp	Pro
65					70				75					80	
Asp	Pro	Asp	His	Pro	Gly	Thr	Ser	Tyr	Thr	Ser	Gln	Gly	Gly	Phe	Leu
				85					90					95	
Arg	Gly	Ala	Gly	Leu	Phe	Asp	Ala	Gly	Leu	Phe	Gly	Ile	Ser	Pro	Arg

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100	105	110
Glu Ala Leu Val Met Asp Pro Gln Gln Arg Val Leu Leu Glu Thr Ser		
115	120	125
Trp Glu Ala Leu Glu Asp Ala Gly Val Asp Pro Leu Ser Leu Lys Gly		
130	135	140
Ser Asp Val Gly Val Phe Ser Gly Val Phe Thr Gln Gly Tyr Gly Ala		
145	150	155
Gly Ala Ile Thr Pro Asp Leu Glu Ala Phe Ala Gly Ile Gly Ala Ala		
165	170	175
Ser Ser Val Ala Ser Gly Arg Val Ser Tyr Val Phe Gly Leu Glu Gly		
180	185	190
Pro Ala Val Thr Ile Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Ile		
195	200	205
His Leu Ala Ala Gln Ala Leu Arg Ala Gly Glu Cys Ser Met Ala Leu		
210	215	220
Ala Gly Gly Ala Thr Val Met Pro Thr Pro Gly Thr Phe Val Ala Phe		
225	230	235
Ser Arg Gln Arg Val Leu Ala Ala Asp Gly Arg Ser Lys Ala Phe Ser		
245	250	255
Ser Thr Ala Asp Gly Thr Gly Trp Ala Glu Gly Ala Gly Val Leu Val		
260	265	270
Leu Glu Arg Leu Ser Val Ala Gln Glu Arg Gly His Arg Ile Leu Ala		
275	280	285
Val Leu Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu		
290	295	300

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Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Lys Ala Leu
305 310 315 320

Ala Gly Ala Gly Leu Val Ala Ser Asp Val Asp Val Val Glu Ala His
325 330 335

Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu
340 345 350

Ala Thr Tyr Gly Gln Gly Arg Glu Arg Pro Leu Trp Leu Gly Ser Val
355 360 365

Lys Ser Asn Phe Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val
370 375 380

Ile Lys Met Val Gln Ala Leu Arg His Gly Ala Met Pro Pro Thr Leu
385 390 395 400

His Val Ala Glu Pro Thr Pro Glu Val Asp Trp Ser Ala Gly Ala Val
405 410 415

Glu Leu Leu Thr Glu Pro Arg Glu Trp Pro Ala Gly Asp Arg Pro Arg
420 425 430

Arg Ala Gly Val Ser Ala Phe Gly Ile Ser Gly Thr Asn Ala His Leu
435 440 445

Ile Leu Glu Glu Ala Pro Pro Ala Asp Ala Val Ala Glu Glu Pro Glu
450 455 460

Phe Lys Gly Pro Val Pro Leu Val Val Ser Ala Gly Ser Pro Thr Ser
465 470 475 480

Leu Ala Ala Gln Ala Gly Arg Leu Ala Glu Val Leu Ala Ser Gly Gly
485 490 495

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Val Ser Arg Ala Arg Leu Ala Ser Gly Leu Leu Ser Gly Arg Ala Leu
 500 505 510

Leu Gly Asp Arg Ala Val Val Val Ala Gly Thr Asp Glu Asp Ala Val
 515 520 525

Ala Gly Leu Arg Ala Leu Ala Arg Gly Asp Arg Ala Pro Gly Val Leu
 530 535 540

Thr Gly Ser Ala Lys His Gly Lys Val Val Tyr Val Phe Pro Gly Gln
 545 550 555 560

Gly Ser Gln Arg Leu Gly Met Gly Arg Glu Leu Tyr Asp Arg Tyr Pro
 565 570 575

Val Phe Ala Thr Ala Phe Asp Glu Ala Cys Glu Gln Leu Asp Val Cys
 580 585 590

Leu Ala Gly Arg Ala Gly His Arg Val Arg Asp Val Val Leu Gly Glu
 595 600 605

Val Pro Ala Glu Thr Gly Leu Leu Asn Gln Thr Val Phe Thr Gln Ala
 610 615 620

Gly Leu Phe Ala Val Glu Ser Ala Leu Phe Arg Leu Ala Glu Ser Trp
 625 630 635 640

Gly Val Arg Pro Asp Val Val Leu Gly His Ser Ile Gly Glu Ile Thr
 645 650 655

Ala Ala Tyr Ala Ala Gly Val Phe Ser Leu Pro Asp Ala Ala Arg Ile
 660 665 670

Val Ala Ala Arg Gly Arg Leu Met Gln Ala Leu Ala Pro Gly Gly Ala
 675 680 685

Met Val Ala Val Ala Ala Ser Glu Ala Glu Val Ala Glu Leu Leu Gly

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690	695	700
Asp Gly Val Glu Leu Ala Ala Val Asn Gly Pro Ser Ala Val Val Leu		
705	710	715 720
Ser Gly Asp Ala Asp Ala Val Val Ala Ala Ala Ala Arg Met Arg Glu		
	725	730 735
Arg Gly His Lys Thr Lys Gln Leu Lys Val Ser His Ala Phe His Ser		
	740	745 750
Ala Arg Met Ala Pro Met Leu Ala Glu Phe Ala Ala Glu Leu Ala Gly		
	755	760 765
Val Thr Trp Arg Glu Pro Glu Ile Pro Val Val Ser Asn Val Thr Gly		
	770	775 780
Arg Phe Ala Glu Pro Gly Glu Leu Thr Glu Pro Gly Tyr Trp Ala Glu		
	785	790 795 800
His Val Arg Arg Pro Val Arg Phe Ala Glu Gly Val Ala Ala Ala Thr		
	805	810 815
Glu Ser Gly Gly Ser Leu Phe Val Glu Leu Gly Pro Gly Ala Ala Leu		
	820	825 830
Thr Ala Leu Val Glu Glu Thr Ala Glu Val Thr Cys Val Ala Ala Leu		
	835	840 845
Arg Asp Asp Arg Pro Glu Val Thr Ala Leu Ile Thr Ala Val Ala Glu		
	850	855 860
Leu Phe Val Arg Gly Val Ala Val Asp Trp Pro Ala Leu Leu Pro Pro		
	865	870 875 880
Val Thr Gly Phe Val Asp Leu Pro Lys Tyr Ala Phe Asp Gln Gln His		
	885	890 895

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Tyr Trp Leu Gln Pro Ala Ala Gln Ala Thr Asp Ala Ala Ser Leu Gly
 900 905 910

Gln Val Ala Ala Asp His Pro Leu Leu Gly Ala Val Val Arg Leu Pro
 915 920 925

Gln Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Leu Lys Ser His
 930 935 940

Pro Trp Leu Ala Asp His Val Ile Gly Gly Val Val Leu Val Ala Gly
 945 950 955 960

Thr Gly Leu Val Glu Leu Ala Val Arg Ala Gly Asp Glu Ala Gly Cys
 965 970 975

Pro Val Leu Glu Glu Leu Val Ile Glu Ala Pro Leu Val Val Pro Asp
 980 985 990

His Gly Gly Val Arg Ile Gln Val Val Val Gly Ala Pro Gly Glu Thr
 995 1000 1005

Gly Ser Arg Ala Val Glu Val Tyr Ser Leu Arg Glu Asp Ala Gly Ala
 1010 1015 1020

Glu Val Trp Ala Arg His Ala Thr Gly Phe Leu Ala Ala Thr Pro Ser
 1025 1030 1035 1040

Gln His Lys Pro Phe Asp Phe Thr Ala Trp Pro Pro Pro Gly Val Glu
 1045 1050 1055

Arg Val Asp Val Glu Asp Phe Tyr Asp Gly Leu Val Asp Arg Gly Tyr
 1060 1065 1070

Ala Tyr Gly Pro Ser Phe Arg Gly Leu Arg Ala Val Trp Arg Arg Gly
 1075 1080 1085

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Asp Glu Val Phe Ala Glu Val Ala Leu Ala Glu Asp Asp Arg Ala Asp
 1090 1095 1100

Ala Ala Arg Phe Gly Ile His Pro Gly Leu Leu Asp Ala Ala Leu His
 1105 1110 1115 1120

Ala Gly Met Ala Gly Ala Thr Thr Thr Glu Glu Pro Gly Arg Pro Val
 1125 1130 1135

Leu Pro Phe Ala Trp Asn Gly Leu Val Leu His Ala Ala Gly Ala Ser
 1140 1145 1150

Ala Leu Arg Val Arg Leu Ala Pro Ser Gly Pro Asp Ala Leu Ser Val
 1155 1160 1165

Glu Ala Ala Asp Glu Ala Gly Gly Leu Val Val Thr Ala Asp Ser Leu
 1170 1175 1180

Val Ser Arg Pro Val Ser Ala Glu Gln Leu Gly Ala Ala Ala Asn His
 1185 1190 1195 1200

Asp Ala Leu Phe Arg Val Glu Trp Thr Glu Ile Ser Ser Ala Gly Asp
 1205 1210 1215

Val Pro Ala Asp His Val Glu Val Leu Glu Ala Val Gly Glu Asp Pro
 1220 1225 1230

Leu Glu Leu Thr Gly Arg Val Leu Glu Ala Val Gln Thr Trp Leu Ala
 1235 1240 1245

Asp Ala Ala Asp Asp Ala Arg Leu Val Val Val Thr Arg Gly Ala Val
 1250 1255 1260

His Glu Val Thr Asp Pro Ala Gly Ala Ala Val Trp Gly Leu Ile Arg
 1265 1270 1275 1280

Ala Ala Gln Ala Glu Asn Pro Asp Arg Ile Val Leu Leu Asp Thr Asp

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1285	1290	1295
Gly Glu Val Pro Leu Gly Arg Val Leu Ala Thr Gly Glu Pro Gln Thr		
1300	1305	1310
Ala Val Arg Gly Ala Thr Leu Phe Ala Pro Arg Leu Ala Arg Ala Glu		
1315	1320	1325
Ala Ala Glu Ala Pro Ala Val Thr Gly Gly Thr Val Leu Ile Ser Gly		
1330	1335	1340
Ala Gly Ser Leu Gly Ala Leu Thr Ala Arg His Leu Val Ala Arg His		
1345	1350	1355
1360		
Gly Val Arg Arg Leu Val Leu Val Ser Arg Arg Gly Pro Asp Ala Asp		
1365	1370	1375
Gly Met Ala Glu Leu Thr Ala Glu Leu Ile Ala Gln Gly Ala Glu Val		
1380	1385	1390
Ala Val Val Ala Cys Asp Leu Ala Asp Arg Asp Gln Val Arg Val Leu		
1395	1400	1405
Leu Ala Glu His Arg Pro Asn Ala Val Val His Thr Ala Gly Val Leu		
1410	1415	1420
Asp Asp Gly Val Phe Glu Ser Leu Thr Arg Glu Arg Leu Ala Lys Val		
1425	1430	1435
1440		
Phe Ala Pro Lys Val Thr Ala Ala Asn His Leu Asp Glu Leu Thr Arg		
1445	1450	1455
Glu Leu Asp Leu Arg Ala Phe Val Val Phe Ser Ser Ala Ser Gly Val		
1460	1465	1470
Phe Gly Ser Ala Gly Gln Gly Asn Tyr Ala Ala Ala Asn Ala Tyr Leu		
1475	1480	1485

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Asp Ala Val Val Ala Asn Arg Arg Ala Ala Gly Leu Pro Gly Thr Ser
 1490 1495 1500

Leu Ala Trp Gly Leu Trp Glu Gln Thr Asp Gly Met Thr Ala His Leu
 1505 1510 1515 1520

Gly Asp Ala Asp Gln Ala Arg Ala Ser Arg Gly Gly Val Leu Ala Ile
 1525 1530 1535

Ser Pro Ala Glu Gly Met Glu Leu Phe Asp Ala Ala Pro Asp Gly Leu
 1540 1545 1550

Val Val Pro Val Lys Leu Asp Leu Arg Lys Thr Arg Ala Gly Gly Thr
 1555 1560 1565

Val Pro His Leu Leu Arg Gly Leu Val Arg Pro Gly Arg Gln Gln Ala
 1570 1575 1580

Arg Pro Ala Ser Thr Val Asp Asn Gly Leu Ala Gly Arg Leu Ala Gly
 1585 1590 1595 1600

Leu Ala Pro Ala Glu Gln Glu Ala Leu Leu Leu Asp Val Val Arg Thr
 1605 1610 1615

Gln Val Ala Leu Val Leu Gly His Ala Gly Pro Glu Ala Val Arg Ala
 1620 1625 1630

Asp Thr Ala Phe Lys Asp Thr Gly Phe Asp Ser Leu Thr Ser Val Glu
 1635 1640 1645

Leu Arg Asn Arg Leu Arg Glu Ala Ser Gly Leu Lys Leu Pro Ala Thr
 1650 1655 1660

Leu Val Phe Asp Tyr Pro Thr Pro Val Ala Leu Ala Arg Tyr Leu Arg
 1665 1670 1675 1680

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Asp Glu Leu Gly Asp Thr Val Ala Thr Thr Pro Val Ala Thr Ala Ala
 1685 1690 1695

Ala Ala Asp Ala Gly Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg
 1700 1705 1710

Leu Pro Gly Gly Val Thr Asp Pro Glu Gly Leu Trp Arg Leu Val Arg
 1715 1720 1725

Asp Gly Leu Glu Gly Leu Ser Pro Phe Pro Glu Asp Arg Gly Trp Asp
 1730 1735 1740

Leu Glu Asn Leu Phe Asp Asp Asp Pro Asp Arg Ser Gly Thr Thr Tyr
 1745 1750 1755 1760

Thr Ser Arg Gly Gly Phe Leu Asp Gly Ala Gly Leu Phe Asp Ala Gly
 1765 1770 1775

Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln
 1780 1785 1790

Arg Leu Leu Leu Glu Ala Ala Trp Glu Ala Leu Glu Gly Thr Gly Val
 1795 1800 1805

Asp Pro Gly Ser Leu Lys Gly Ala Asp Val Gly Val Phe Ala Gly Val
 1810 1815 1820

Ser Asn Gln Gly Tyr Gly Met Gly Ala Asp Pro Ala Gln Leu Ala Gly
 1825 1830 1835 1840

Tyr Ala Ser Thr Ala Gly Ala Ser Ser Val Val Ser Gly Arg Val Ser
 1845 1850 1855

Tyr Val Phe Gly Phe Glu Gly Pro Ala Val Thr Ile Asp Thr Ala Cys
 1860 1865 1870

Ser Ser Ser Leu Val Ala Met His Leu Ala Gly Gln Ala Leu Arg Gln

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1875	1880	1885
Gly Glu Cys Ser Met Ala Leu Ala Gly Gly Val Thr Val Met Gly Thr		
1890	1895	1900
Pro Gly Thr Phe Val Glu Phe Ala Lys Gln Arg Gly Leu Ala Gly Asp		
1905	1910	1915
		1920
Gly Arg Cys Lys Ala Tyr Ala Glu Gly Ala Asp Gly Thr Gly Trp Ala		
1925	1930	1935
Glu Gly Val Gly Val Val Val Leu Glu Arg Leu Ser Val Ala Arg Glu		
1940	1945	1950
Arg Gly His Arg Val Leu Ala Val Leu Arg Gly Ser Ala Val Asn Ser		
1955	1960	1965
Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln		
1970	1975	1980
Arg Val Ile Arg Arg Ala Leu Ala Gly Ala Gly Leu Glu Pro Ser Asp		
1985	1990	1995
		2000
Val Asp Ile Val Glu Gly His Gly Thr Gly Thr Ala Leu Gly Asp Pro		
2005	2010	2015
Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Lys Asp Arg Asp Pro		
2020	2025	2030
Glu Thr Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Phe Gly His Thr		
2035	2040	2045
Gln Ser Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Gln Ala Leu		
2050	2055	2060
Arg His Gly Val Met Pro Pro Thr Leu His Val Asp Arg Pro Thr Ser		
2065	2070	2075
		2080

Gln Val Asp Trp Ser Ala Gly Ala Val Glu Val Leu Thr Glu Ala Arg
 2085 2090 2095

Glu Trp Pro Arg Asn Gly Arg Pro Arg Arg Ala Gly Val Ser Ser Phe
 2100 2105 2110

Gly Ile Ser Gly Thr Asn Ala His Leu Ile Ile Glu Glu Ala Pro Ala
 2115 2120 2125

Glu Pro Gln Leu Ala Gly Pro Pro Pro Asp Gly Gly Val Val Pro Leu
 2130 2135 2140

Val Val Ser Ala Arg Ser Pro Gly Ala Leu Ala Gly Gln Ala Arg Arg
 2145 2150 2155 2160

Leu Ala Thr Phe Leu Gly Asp Gly Pro Leu Ser Asp Val Ala Gly Ala
 2165 2170 2175

Leu Thr Ser Arg Ala Leu Phe Gly Glu Arg Ala Val Val Val Ala Asp
 2180 2185 2190

Ser Ala Glu Glu Ala Arg Ala Gly Leu Gly Ala Leu Ala Arg Gly Glu
 2195 2200 2205

Asp Ala Pro Gly Leu Val Arg Gly Arg Val Pro Ala Ser Gly Leu Pro
 2210 2215 2220

Gly Lys Leu Val Trp Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly
 2225 2230 2235 2240

Met Gly Arg Glu Leu Leu Glu Glu Ser Pro Val Phe Ala Glu Arg Ile
 2245 2250 2255

Ala Glu Cys Ala Ala Ala Leu Glu Pro Trp Ile Gly Trp Ser Leu Phe
 2260 2265 2270

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Asp Val Leu Arg Gly Asp Gly Asp Leu Asp Arg Val Asp Val Leu Gln
 2275 2280 2285

Pro Ala Cys Phe Ala Val Met Val Gly Leu Ala Ala Val Trp Ser Ser
 2290 2295 2300

Ala Gly Val Val Pro Asp Ala Val Leu Gly His Ser Gln Gly Glu Ile
 2305 2310 2315 2320

Ala Ala Ala Cys Val Ser Gly Ala Leu Ser Leu Glu Asp Ala Ala Lys
 2325 2330 2335

Val Val Ala Leu Arg Ser Gln Ala Ile Ala Ala Lys Leu Ser Gly Arg
 2340 2345 2350

Gly Gly Met Ala Ser Val Ala Leu Gly Glu Ala Asp Val Val Ser Arg
 2355 2360 2365

Leu Ala Asp Gly Val Glu Val Ala Ala Val Asn Gly Pro Ala Ser Val
 2370 2375 2380

Val Ile Ala Gly Asp Ala Gln Ala Leu Asp Glu Thr Leu Glu Ala Leu
 2385 2390 2395 2400

Ser Gly Ala Gly Ile Arg Ala Arg Arg Val Ala Val Asp Tyr Ala Ser
 2405 2410 2415

His Thr Arg His Val Glu Asp Ile Glu Asp Thr Leu Ala Glu Ala Leu
 2420 2425 2430

Ala Gly Ile Asp Ala Arg Ala Pro Leu Val Pro Phe Leu Ser Thr Leu
 2435 2440 2445

Thr Gly Glu Trp Ile Arg Asp Glu Gly Val Val Asp Gly Gly Tyr Trp
 2450 2455 2460

Tyr Arg Asn Leu Arg Gly Arg Val Arg Phe Gly Pro Ala Val Glu Ala

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2465	2470	2475	2480
Leu Leu Ala Gln Gly His Gly Val Phe Val Glu Leu Ser Ala His Pro			
2485	2490	2495	
Val Leu Val Gln Pro Ile Thr Glu Leu Thr Asp Glu Thr Ala Ala Val			
2500	2505	2510	
Val Thr Gly Ser Leu Arg Arg Asp Asp Gly Gly Leu Arg Arg Leu Leu			
2515	2520	2525	
Thr Ser Met Ala Glu Leu Phe Val Arg Gly Val Glu Val Asp Trp Thr			
2530	2535	2540	
Ser Leu Val Pro Pro Ala Arg Ala Asp Leu Pro Thr Tyr Ala Phe Asp			
2545	2550	2555	2560
His Glu His Tyr Trp Leu Arg Ala Ala Asp Thr Ala Ser Asp Ala Val			
2565	2570	2575	
Ser Leu Gly Leu Ala Gly Ala Asp His Pro Leu Leu Gly Ala Val Val			
2580	2585	2590	
Gln Leu Pro Gln Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Leu			
2595	2600	2605	
Arg Ser His Pro Trp Leu Ala Asp His Ala Val Arg Asp Val Val Ile			
2610	2615	2620	
Val Pro Gly Thr Gly Leu Val Gln Leu Ala Val Arg Ala Gly Asp Glu			
2625	2630	2635	2640
Ala Gly Cys Pro Val Leu Asp Glu Leu Val Ile Glu Ala Pro Leu Val			
2645	2650	2655	
Val Pro Arg Arg Gly Gly Val Arg Val Gln Val Ala Leu Gly Gly Pro			
2660	2665	2670	

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Ala Asp Asp Gly Ser Arg Thr Val Asp Val Phe Ser Leu Arg Glu Asp
 2675 2680 2685

Ala Asp Ser Trp Leu Arg His Ala Thr Gly Val Leu Val Pro Glu Asn
 2690 2695 2700

Arg Pro Arg Gly Thr Ala Ala Phe Asp Phe Ala Ala Trp Pro Pro Pro
 2705 2710 2715 2720

Glu Ala Lys Pro Val Asp Leu Thr Gly Ala Tyr Asp Val Leu Ala Asp
 2725 2730 2735

Val Gly Tyr Gly Tyr Gly Pro Thr Phe Arg Ala Val Arg Ala Val Trp
 2740 2745 2750

Arg Arg Gly Ser Gly Asn Thr Thr Glu Thr Phe Ala Glu Ile Ala Leu
 2755 2760 2765

Pro Glu Asp Ala Arg Ala Glu Ala Gly Arg Phe Gly Ile His Pro Ala
 2770 2775 2780

Leu Leu Asp Ala Ala Leu His Ser Thr Met Val Ser Ala Ala Ala Asp
 2785 2790 2795 2800

Thr Glu Ser Tyr Gly Asp Glu Val Arg Leu Pro Phe Ala Trp Asn Gly
 2805 2810 2815

Leu Arg Leu His Ala Ala Gly Ala Ser Val Leu Arg Val Arg Val Ala
 2820 2825 2830

Lys Pro Glu Arg Asp Ser Leu Ser Leu Glu Ala Val Asp Glu Ser Gly
 2835 2840 2845

Gly Leu Val Val Thr Leu Asp Ser Leu Val Gly Arg Pro Val Ser Asn
 2850 2855 2860

Asp	Gln	Leu	Thr	Thr	Ala	Ala	Gly	Pro	Ala	Gly	Ala	Gly	Ser	Leu	Tyr
2865							2870					2875			2880

Arg	Val	Asp	Trp	Thr	Pro	Leu	Ser	Ser	Val	Asp	Thr	Ser	Gly	Arg	Val
							2885				2890			2895	

Pro	Ser	Trp	Leu	Pro	Val	Ala	Thr	Ala	Glu	Glu	Val	Ala	Thr	Leu	Ala
			2900						2905					2910	

Asp	Asp	Val	Leu	Thr	Gly	Ala	Thr	Glu	Ala	Pro	Ala	Val	Ala	Val	Met
			2915					2920					2925		

Glu	Ala	Val	Ala	Asp	Glu	Gly	Ser	Val	Leu	Ala	Leu	Thr	Val	Arg	Val
	2930					2935							2940		

Leu	Asp	Val	Val	Gln	Cys	Trp	Leu	Ala	Gly	Gly	Gly	Leu	Glu	Gly	Thr
2945						2950					2955				2960

Lys	Leu	Ala	Ile	Val	Thr	Arg	Gly	Ala	Val	Pro	Ala	Gly	Asp	Gly	Val
						2965				2970				2975	

Val	His	Asp	Pro	Ala	Ala	Ala	Ala	Val	Trp	Gly	Leu	Val	Arg	Ala	Ala
			2980						2985					2990	

Gln	Ala	Glu	Asn	Pro	Asp	Arg	Ile	Val	Leu	Leu	Asp	Val	Glu	Pro	Glu
			2995					3000					3005		

Ala	Asp	Val	Pro	Pro	Leu	Leu	Gly	Ser	Val	Leu	Ala	Asp	Gly	Glu	Pro
		3010					3015					3020			

Gln	Val	Ala	Val	Arg	Gly	Thr	Thr	Leu	Ser	Ile	Pro	Arg	Leu	Ala	Arg
3025					3030						3035				3040

Ala	Ala	Arg	Pro	Asp	Pro	Ala	Ala	Gly	Phe	Lys	Thr	Arg	Gly	Pro	Val
					3045				3050					3055	

Leu	Val	Thr	Gly	Gly	Thr	Gly	Ser	Leu	Gly	Gly	Leu	Val	Ala	Arg	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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3060	3065	3070
Leu Val Glu Arg His Gly Val Arg Gln Leu Val Leu Ala Ser Arg Arg		
3075	3080	3085
Gly Leu Asp Ala Glu Gly Ala Lys Asp Leu Val Thr Asp Leu Thr Ala		
3090	3095	3100
Leu Gly Ala Asp Val Ala Val Ala Ala Cys Asp Val Ala Asp Arg Asp		
3105	3110	3115 3120
Gln Val Ala Ala Leu Leu Thr Glu His Arg Pro Ser Ala Val Val His		
3125	3130	3135
Thr Ala Gly Val Pro Asp Ala Gly Val Ile Gly Thr Val Thr Pro Asp		
3140	3145	3150
Arg Leu Ala Glu Val Phe Ala Pro Lys Val Thr Ala Ala Arg His Leu		
3155	3160	3165
Asp Glu Leu Thr Arg Asp Leu Asp Leu Asp Ser Phe Val Val Tyr Ser		
3170	3175	3180
Ser Val Ser Ala Val Phe Met Gly Ala Gly Ser Gly Ser Tyr Ala Ala		
3185	3190	3195 3200
Ala Asn Ala Tyr Leu Asp Gly Leu Met Ala His Arg Arg Ala Ala Gly		
3205	3210	3215
Leu Pro Gly Gln Ser Leu Ala Trp Gly Leu Trp Asp Gln Thr Thr Gly		
3220	3225	3230
Gly Met Ala Ala Gly Thr Asp Glu Ala Gly Arg Ala Arg Met Thr Arg		
3235	3240	3245
Arg Gly Gly Leu Val Ala Met Lys Pro Ala Ala Gly Leu Asp Leu Phe		
3250	3255	3260

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Asp Ala Ala Ile Gly Ser Gly Glu Pro Leu Leu Val Pro Ala Gln Leu
 3265 3270 3275 3280

Asp Leu Arg Gly Leu Arg Ala Glu Ala Ala Gly Gly Thr Glu Val Pro
 3285 3290 3295

His Leu Leu Arg Gly Leu Val Arg Ala Gly Arg Gln Gln Ala Arg Ala
 3300 3305 3310

Ala Ser Thr Val Glu Glu Asn Trp Ala Gly Arg Leu Ala Gly Leu Glu
 3315 3320 3325

Pro Ala Glu Arg Gly Gln Val Leu Leu Glu Leu Val Arg Ala Gln Val
 3330 3335 3340

Ala Gly Val Leu Gly Tyr Arg Ala Ala His Gln Val Asp Pro Asp Gln
 3345 3350 3355 3360

Gly Leu Phe Glu Ile Gly Phe Asp Ser Leu Thr Ala Ile Glu Leu Arg
 3365 3370 3375

Asn Arg Leu Arg Ala Arg Thr Glu Arg Lys Ile Ser Pro Gly Val Val
 3380 3385 3390

Phe Asp His Pro Thr Pro Ala Leu Leu Ala Ala His Leu Asn Glu Leu
 3395 3400 3405

Leu Arg Lys Lys Val
 3410

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met	Ala	Ile	Pro	Tyr	Ser	Ser	Leu	Ala	Tyr	Glu	Leu	Arg	Asp	Ala	Val
1			5						10					15	

Asn	Val	Val	Asp	Leu	Asp	Glu	Asp	Asp	Val	Phe	Val	Thr	Ser	Ile	Ala
			20					25					30		

Glu	Gly	Gln	Gly	Gly	Ala	Cys	Tyr	His	Leu	Asn	Arg	Leu	Phe	His	Arg
		35					40						45		

Leu	Leu	Thr	Glu	Leu	Gly	Tyr	Asp	Val	Thr	Pro	Leu	Ala	Gly	Ser	Thr
		50					55				60				

Ala	Glu	Gly	Arg	Glu	Thr	Phe	Gly	Thr	Asp	Val	Glu	His	Met	Phe	Asn
65						70				75				80	

Leu	Val	Thr	Leu	Asp	Gly	Ala	Asp	Trp	Leu	Val	Asp	Val	Gly	Tyr	Pro
			85					90						95	

Gly	Pro	Thr	Tyr	Val	Glu	Pro	Leu	Ala	Val	Ser	Pro	Ala	Val	Gln	Thr
			100					105					110		

Gln	Tyr	Gly	Ser	Gln	Phe	Arg	Leu	Val	Glu	Gln	Glu	Thr	Gly	Tyr	Ala
			115				120						125		

Leu	Gln	Arg	Arg	Gly	Ala	Val	Thr	Arg	Trp	Ser	Val	Val	Tyr	Thr	Phe
		130					135						140		

Thr	Thr	Gln	Pro	Arg	Gln	Trp	Ser	Asp	Trp	Lys	Glu	Leu	Glu	Asp	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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145	150	155	160
Phe Arg Ala Leu Val Gly Asp Thr Thr Arg Thr Asp Thr Gln Glu Thr			
165	170	175	
Leu Cys Gly Arg Ala Phe Ala Asn Gly Gln Val Phe Leu Arg Gln Arg			
180	185	190	
Arg Tyr Leu Thr Val Glu Asn Gly Arg Glu Gln Val Arg Thr Ile Thr			
195	200	205	
Asp Asp Asp Glu Phe Arg Ala Leu Val Ser Arg Val Leu Ser Gly Asp			
210	215	220	
His Gly			
225			

Ciba-Geigy AG

CH-4002 Basel

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: pR17-3	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 11114
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
<p>The microorganism identified under I. above was accompanied by:</p> <p>(X) a scientific description (X) a proposed taxonomic designation</p> <p>(Mark with a cross where applicable).</p>	
III. RECEIPT AND ACCEPTANCE	
This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on 1996-08-10 (Date of the original deposit).	
IV. RECEIPT OF REQUEST FOR CONVERSION	
The microorganism identified under I. above was received by this International Depositary Authority on (date of original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
<p>Name: DSMZ-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH</p> <p>Address: Marchfelder Weg 1b D-38124 Braunschweig</p>	<p>Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):</p> <p><i>V. Weiler</i></p> <p>Date: 1996-08-14</p>

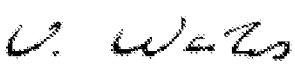
¹ Where Rule 6.4 (d) applies, such date is the date on which the status of international depositary authority was acquired.

Ciba-Geigy AG

CH-4002 Basel

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: Ciba-Geigy AG Address: CH-4002 Basel	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY DSM 11114 Date of the deposit or the transfer: 1996-08-10
III. VIABILITY STATEMENT	
The viability of the microorganism identified under II above was tested on 1996-08-12. On that date, the said microorganism was <input checked="" type="checkbox"/> (X) viable <input type="checkbox"/> () no longer viable	
IV. CONDITIONS UNDER WHICH THE VIABILITY TEST HAS BEEN PERFORMED	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: DSMZ-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH Address: Mascheroder Weg 1b D-38124 Braunschweig	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s)  Date: 1996-08-14

- * Indicate the date of original deposit or, where a new deposit or a transfer has been made, the most recent relevant date (date of the new deposit or date of the transfer).
- * In the cases referred to in Rule 10.2(a) (ii) and (iii), refer to the most recent viability test.
- * Mark with a cross the applicable box.
- * Fill in if the information has been requested and if the results of the test were negative.

Novartis AG

CH-4002 Basel

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: pR144-2	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 11655
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
<p>The microorganism identified under I. above was accompanied by:</p> <p><input checked="" type="checkbox"/> a scientific description</p> <p><input checked="" type="checkbox"/> a proposed taxonomic designation</p> <p>(Mark with a cross where applicable).</p>	
III. RECEIPT AND ACCEPTANCE	
<p>This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on 1997-07-14 (Date of the original deposit).</p>	
IV. RECEIPT OF REQUEST FOR CONVERSION	
<p>The microorganism identified under I. above was received by this International Depositary Authority on (date of original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).</p>	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
<p>Name: DSMZ-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH</p> <p>Address: Mascheroder Weg 1b D-38124 Braunschweig</p>	<p>Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):</p> <p><i>V. Weh</i></p> <p>Date: 1997-07-15</p>

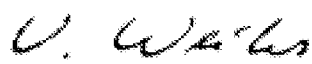
¹ Where Rule 6.4 (d) applies, such date is the date on which the status of international depositary authority was acquired.

Novartis AG

CH-4002 Basel

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

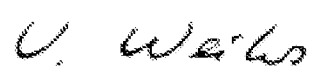
I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: Novartis AG Address: CH-4002 Basel	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 11655 Date of the deposit or the transfer: 1997-07-14
III. VIABILITY STATEMENT	
The viability of the microorganism identified under II above was tested on 1997-07-14. On this date, the said microorganism was <input checked="" type="checkbox"/> (X) viable <input type="checkbox"/> () no longer viable	
IV. CONDITIONS UNDER WHICH THE VIABILITY TEST HAS BEEN PERFORMED ¹	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: DSMZ-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH Address: Mascheroder Weg 1b D-38124 Braunschweig	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):  Date: 1997-07-15

- ¹ Indicate the date of original deposit or, where a new deposit or a transfer has been made, the most recent relevant date (date of the new deposit or date of the transfer).
- ² In the cases referred to in Rule 10.2(a) (ii) and (iii), refer to the most recent viability test.
- ³ Mark with a cross the applicable box.
- ⁴ Fill in if the information has been requested and if the results of the test were negative.

Novartis AG

CH-4002 Basel

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: pNE95	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 11656
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
The microorganism identified under I. above was accompanied by: <input checked="" type="checkbox"/> a scientific description <input checked="" type="checkbox"/> a proposed taxonomic designation (Mark with a cross where applicable).	
III. RECEIPT AND ACCEPTANCE	
This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on 1997-07-14 (Date of the original deposit).	
IV. RECEIPT OF REQUEST FOR CONVERSION	
The microorganism identified under I. above was received by this International Depositary Authority on (date of original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: DSMZ-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH Address: Mascheroder Weg 1b D-38124 Braunschweig	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):  Date: 1997-07-15


¹ Where Rule 6.4 (d) applies, such date is the date on which the status of international depositary authority was acquired.

Novartis AG

CH-4002 Basel

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: Novartis AG Address: CH-4002 Basel	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 11656 Date of the deposit or the transfer: 1997-07-14
III. VIABILITY STATEMENT	
The viability of the microorganism identified under II above was tested on 1997-07-14. On that date, the said microorganism was <input checked="" type="checkbox"/> (X) viable <input type="checkbox"/> () no longer viable	
IV. CONDITIONS UNDER WHICH THE VIABILITY TEST HAS BEEN PERFORMED*	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: DSMZ-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH Address: Marchfelder Weg 1b D-38124 Braunschweig	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):  Date: 1997-07-15

* Indicate the date of original deposit or, where a new deposit or a transfer has been made, the most recent relevant date (date of the new deposit or date of the transfer).

* In the cases referred to in Rule 10.2(a) (ii) and (iii), refer to the most recent viability test.


* Mark with a cross the applicable box.

* Fill in if the information has been requested and if the results of the test were negative.

Novartis AG

CH-4002 Basel

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.3 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: pNE112	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 11657
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
<p>The microorganism identified under I. above was accompanied by:</p> <p><input type="checkbox"/> a scientific description</p> <p><input checked="" type="checkbox"/> a proposed taxonomic designation</p> <p>(Mark with a cross where applicable).</p>	
III. RECEIPT AND ACCEPTANCE	
<p>This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on 1997-07-14 (Date of the original deposit).</p>	
IV. RECEIPT OF REQUEST FOR CONVERSION	
<p>The microorganism identified under I. above was received by this International Depositary Authority on (date of original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).</p>	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
<p>Name: DSMZ-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH</p> <p>Address: Mascheroder Weg 1b D-38124 Braunschweig</p>	<p>Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s).</p> <p></p> <p>Date: 1997-07-15</p>


¹ Where Rule 6.4 (d) applies, such date is the date on which the status of international depositary authority was acquired.

Novartis AG

CH-4002 Basel

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: Novartis AG Address: CH-4002 Basel	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 11657 Date of the deposit or the transfer: 1997-07-14
III. VIABILITY STATEMENT	
The viability of the microorganism identified under II above was tested on 1997-07-14. On that date, the said microorganism was <input checked="" type="checkbox"/> (X) viable <input type="checkbox"/> () no longer viable	
IV. CONDITIONS UNDER WHICH THE VIABILITY TEST HAS BEEN PERFORMED	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: DSMZ-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH Address: Marchfelder Weg 1b D-38124 Braunschweig	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s).  Date: 1997-07-15

* Indicate the date of original deposit or, where a new deposit or a transfer has been made, the most recent relevant date (date of the new deposit or date of the transfer).

* In the cases referred to in Rule 10.2(a) (ii) and (iii), refer to the most recent viability test.

* Mark with a cross the applicable box.

* Fill in if the information has been requested and if the results of the test were negative.

What is claimed is:

1. A DNA fragment from the genome of *Ammycolatopsis mediterranei* which comprises a DNA region which is involved directly or indirectly in the gene cluster responsible for rifamycin synthesis, including the adjacent DNA regions to the right and left which, by reason of their function in connection with rifamycin biosynthesis, qualify as constituent of this rifamycin gene cluster; and functional fragments, derivatives or constituents thereof.
2. A DNA fragment according to claim 1, which is directly or indirectly involved in the gene cluster responsible for rifamycin synthesis.
3. A DNA fragment according to claim 1, which comprises sequence portions which code for a polyketide synthase or an enzymatically active domain thereof.
4. A DNA fragment according to claim 1, which comprises SEQ ID NO 1 or SEQ ID NO 3 or at least 15 consecutive nucleotides therefrom.
5. A DNA fragment according to claim 1, wherein said fragment comprises one or more of the partial nucleotide sequences depicted in SEQ ID NOS 1 and/or 3, or functional fragments thereof, and all other DNA sequences in the vicinity of this sequence which can, by reason of homologies which are present, be regarded as structural or functional equivalents and are therefore able to hybridize with this sequence.
6. A DNA fragment according to claim 1, wherein said fragment comprises a nucleotide sequence selected from the group consisting of ORF A, B, C, D, E and F or functional fragments thereof, or encodes one or more of the proteins or polypeptides, or functional derivatives thereof, depicted in SEQ ID NOS 4 to 9.
7. A method for identifying, isolating and cloning a DNA fragment according to claim 1.

8. A method according to claim 7, which comprises the following steps:
 - setting up of a genomic gene bank,
 - screening of this gene bank with the assistance of the DNA sequences according to the invention, and
 - isolation of the clones identified as positive.
9. The use of a DNA fragment according to claim 1 in the production of ansamycins or precursors thereof; including those in which the aliphatic bridge is connected only at one end to the aromatic nucleus.
10. The use of a DNA fragment according to claim 1 in the production of rifamycin, rifamycin analogues or precursors thereof.
11. The use of a DNA fragment according to claim 1 for inactivating or modifying genes of ansamycin biosynthesis.
12. The use of a DNA fragment according to claim 1 for inactivating or modifying genes of rifamycin biosynthesis, or the biosynthesis of rifamycin analogues.
13. The use of a DNA fragment according to claim 1 for constructing mutated actinomycetes strains from which the natural rifamycin or ansamycin biosynthesis gene cluster in the chromosome has been partly or completely deleted.
14. The use of DNA fragments according to claim 1 for assembling a library of polyketide synthases.
15. The use of the polyketide synthases according to claim 14 for assembling a library of polyketides.
16. A polyketide synthase from *Amycolatopsis mediterranei* which is directly or indirectly involved in rifamycin synthesis; and functional constituents or domains thereof.

17. The use of the polyketide synthase according to claim 16 for synthesizing ansamycins.
18. The use of polyketide synthases according to claim 14 for synthesizing a library of ansamycins.
19. A hybrid vector comprising a DNA fragment according to claim 1.
20. A hybrid vector comprising an expression vector comprising a DNA fragment according to claim 1.
21. A host organism comprising a hybrid vector according to claim 19.
22. A hybridization probe comprising a DNA fragment according to claim 1.
23. The use of the hybridization probe according to claim 22 for identifying DNA fragments involved in the biosynthesis of ansamycins.

INTERNATIONAL SEARCH REPORT

In national Application No.

PCT/EP 97/04495

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/52 C12P17/18 C12P17/10 C12N9/00 C12N1/21
C12N15/70 C1201/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C12P

Documentation searched other than minimum documentation to the extent that such documents are excluded in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	LAL, R. ET AL: "Rifamycins: strain improvement program" CRIT. REV. MICROBIOL. (1995), 21(1), 19-30 CODEN: CRYMAC; ISSN: 1040-841X, XP000615990 see the whole document	1
Y	MADON J ET AL: "TRANSFORMATION SYSTEM FOR AMYCOLATOPSIS -MEDITERRANEI DIRECT TRANSFORMATION OF MYCELIUM WITH PLASMID DNA." J BACTERIOL 173 (20), 1991, 6325-6331. CODEN: JOBAAY ISSN: 0021-9193, XP000615993 see the whole document	1
A	WO 87 03907 A (LUBRIZOL GENETICS INC) 2 July 1987 see claims	1



Further documents are listed in the continuation of box C



Patent family members are listed in annex

Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another claim or other special reason (as specified)
- "O" document relating to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the practice or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "8" document member of the same patent family

Date of the actual completion of the international search:

7 January 1998

Date of making of the international search report

13/01/1998

Name and mailing address of the ISA

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Authorized official

Delanghe, L

INTERNATIONAL SEARCH REPORT

In: International Application No.

PCT/EP 97/04495

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication where appropriate, of the relevant passages	Relevant to claim No.
A	<p>WO 95 08548 A (UNIV LELAND STANFORD JUNIOR ;JOHN INNES CENTRE (GB)) 30 March 1995 see claims</p>	1

INTERNATIONAL SEARCH REPORT

Information on patent family members

Int. Patent Application No.

PCT/EP 97/04495

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 8703907 A	02-07-87	AU 598516 B	28-06-90
		AU 6835487 A	15-07-87
		EP 0262154 A	06-04-88
		EP 0463707 A	02-01-92
WO 9508548 A	30-03-95	US 5672491 A	30-09-97
		AU 678058 B	15-05-97
		AU 7731794 A	10-04-95
		CA 2171629 A	30-03-95
		EP 0725778 A	14-08-96
		JP 9505983 T	17-06-97